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(57) Abstract

The present invention introduces a new approach to optimization problems based on a previous theoretical work on extinction patterns in macroevolution. We name them Macroevolutionary Algorithms (MA). Unlike population-level evolution, which is employed in standard genetic algorithms, evolution at the level of higher taxa is used as the underlying metaphor. The model exploits the presence of links between "species" which represent candidate solutions to the optimization problem. In order to test its effectiveness, we compared the performance of MAs versus genetic algorithms (GA) with tournament selection. The method is shown to be a good alternative to standard GAs, showing a fast monotonous search over the solution space even for very small population sizes. A mean field theoretical approach is presented, showing that the basic dynamics of MAs is close to an ecological model of multispecies competition.

(57) Abrégé

L'invention concerne une nouvelle technique d'approche des problèmes d'optimisation, en fonction d'un travail antérieur effectué sur des configurations d'extinction en macroévolution, désignées algorithmes macroévolutifs (MA). Par opposition à l'évolution du niveau de la population, utilisée dans les algorithmes génétiques (GA) standards, on utilise l'évolution à un niveau taxinomique plus élevé sous forme d'une métaphore sous-jacente. Ladite technique exploite la présence de liaisons entre les espèces, représentant des solution candidates au problème de l'optimisation. Afin de tester l'efficacité de cette technique, on compare la performance des MA par rapport aux GA avec une sélection de tournoi. Cette technique s'avère constituer une bonne alternative aux GA standards, par réalisation d'une recherche monotone rapide dans l'espace de solution, même pour des dimensions de population très limitées. L'approche théorique présentée montre que les forces dynamiques de base des MA sont proches d'un modèle écologique de compétition entre espèces multiples.

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The present invention introduces a new approach to optimization problems based on a previous theoretical work on extinction patterns in macroevolution. We name them Macroevolutionary Algorithms (MA). Unlike population-level evolution, which is employed in standard genetic algorithms, evolution at the level of higher taxa is used as the underlying metaphor. The model exploits the presence of links between "species" which represent candidate solutions to the optimization problem. In order to test its effectiveness, we compared the performance of MAs versus genetic algorithms (GA) with tournament selection. The method is shown to be a good alternative to standard GAs, showing a fast monotonous search over the solution space even for very small population sizes. A mean field theoretical approach is presented, showing that the basic dynamics of MAs is close to an ecological model of multispecies competition.

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Description

A METHOD AND SYSTEM FOR PERFORMING OPTIMIZATION ON FITNESS LANDSCAPES

1 Field of the Invention

The present invention relates generally to performing optimization on fitness landscapes using macroevolutionary algorithms. More particularly, the present invention comprises species to represent candidate solutions to the optimization problem and a plurality of rules and operators that govern the extinction and colonization of species.

2 Background

Evolutionary computataion[1] comprises techniques that has been inspired in biological mechanisms of evolution to develop strategies for solving optimization problems[6]. The search takes place often on a rugged landscape which is a geometric representation of the optimality of all possible solutions[5]. Populations of individuals (candidate solution to a given problem) evolve using operators inspired in the theory of evolution by natural selection.

In genetic algorithms (GA)[3, 2, 5], populations are formed by a constant number of individuals N described by B-bit sequences. From a given population at a given generation, the next generation is obtained by applying the *selection operator* followed by the *crossover operator* and the *mutation operator*. In standard GA, the selection operator chooses individuals with a probability proportional to its fitness, but this can sometimes lead to premature convergence. In this sense, the selection operator strongly constrains the convergence velocity of evolutionary algorithms. To avoid these problems, other operators such as rank selection or tournament selection can be used [5]. Next, pairs of individuals are randomly combined with a crossover probability p_c by randomly choosing the crossover point. Finally, each bit of each individual is mutated with a mutation probability p_m[5].

As a result of their simplicity and flexibility, GA's can be applied to a large set of combinational optimization problems with a large space of candidate solutions,

although the intrinsic metastability that characterizes their dynamics has been only recently understood in theoretical terms. In optimization problems with several local extrema, the GA's are widely used because of its general purpose to find a good approximation[5]. However, instead of the Darwinian, short-term evolutionary metaphor, a different time scale can be considered, the macroevolutionary one, where extinctions and diversification of species through internal interactions are at work. Large extinctions can generate coherent population responses very different from the slow, Darwinian dynamics of classical GA. Besides, the population of candidate solutions/species might be understood in terms of an ecological system with connections among different species, instead of just a number of independent entities with a given assigned fitness value.

In this paper, a simple model of macroevolution will be used as a starting point to solve global-extremization problems. Our method will be called a macroevolutionary algorithm (MA) and it will be compared with GA's through some statistical measures obtained from numerical experiments with seven standard multivalued functions. A theoretical approach to a specific (though relevant) case will be considered in order to understand the dynamics of this system. It will be shown that the basic mechanism involves competition among fitness peaks with an eventual symmetry-breaking process if two peaks are identical or very close in fitness.

3 Brief Description of Drawings

FIG. 1 shows a vector field in the (N^k, N^r)-space for the mean-field theory of the two-peak MA problem, as defined by equations (19-20). Here we use $\eta = 0.5$, $\xi = 0.01$, $P = 1$, $D = 1$, $r = 0.01$. The system flows towards a single attractor $(F, 0)$ which is globally stable.

FIG. 2 shows a shows a vector field in the (N^k, N^r) -space for the mean-field theory of the two-peak MA problem for the marginal problem $\eta = 0$ (two identical peaks). Here the system is described by a couple of linear equations (21-22) which lead to an infinite number of stable solutions, as given by the line $N^r = 1 - N^k$.

FIG. 3 shows a landscape of two 2-input functions. FIG 4. shows four stages in the evolution of population applying MA to example 1 ($P = 50, G = 100$.) Each $\circ$ indicates an individual represented in input space, Δ are local maxima.

FIG. 5 shows four stages in the evolution of population applying MA to example 2 ($P = 50, G = 100$). Each $\circ$ indicates an individual represented in input space, Δ.

FIG. 6 shows a parameter behavior for the MA in example 1 (6A, 6B, 6C) and example 2 (6D, 6E, 6F). ($G = 400, P = 50, R = 50$.)

FIG. 7 shows a mean fitness value about all population in each generation for a run ($G = 100, P = 100$ for GA and $P = 50$ for MA.)

FIG. 8 shows the best individual fitness in each generation for three runs using example 1 (8A, 8B) and example 2 (8C,8D). ($G = 100, P = 100$ for GA and $P = 50$ for MA.)

FIG. 9 shows different measures according to population size for both GA and MA for example 1 (9A, 9C) and example 2. (10B) ($P$from 50 to 400 step 10, $G = 400$, $R = 50$.)

FIG. 10 shows a relation between fitness value reached, probability of success to reach a good fitness, and time required, applying GA and MA to examples 1 (10A) and 2 (10B).

FIGS. 11a–11d shows a relation between fitness value reached and time needed, applying GA and MA to examples 2 to 6.

FIGS. 12a-b shows a relation between fitness value reached and time needed, applying GA and MA to examples 7 and 8.

FIG. 13 discloses a representative computer system 1310 in conjunction with which the embodiments of the present invention may be implemented.

Detailed Description of the Preferred Embodiment

4 Model of Macroevolution

The biological model of macroevolution (MM) [8] allows to stimulate the dynamics of species extinction and diversification for large time scales[8, 10]. The model used in our study is a network ecosystem where the dynamics is based only on the relation between species. The links between units/species are essential to determine the new state (alive or extinct) of each species at each generation. We can define the state of species i in the generation t as

$$S_i(t) = \begin{cases} 1 & \text{if state is "alive"} \\ 0 & \text{if state is "extinct"} \end{cases} \tag{1}$$

Moreover, the model considers that time is discretized in "generations" and that each generation is constituted by a set of P species where P is constant. The relationship between species is represented by a connectivity matrix W, where each item $W_{i,j}(t)$ $(i, j \in \{1, \ldots, P\})$ measures the influence of species j on species i at t with a continuous value within the interval $[-1, +1]$ (in ecology, this influence is interpreted as the trophic relation between species). At the end of each generation, all extinct species will be replaced by the species. Briefly, each generation in the

biological model consists on a set of steps (the rules) which will be translated to the MA model (see below):

1. *Random variation*: For each species i, a connection $W_{i,j}(t)$ is randomly chosen, and a new random value between -1 and 1 is assigned.

2. *Extinction*: The relation of each species with the rest of the population determines its survival coefficient h defined as

$$h_i(t) = \sum_{j=1}^{P} W_{i,j}(t) \tag{2}$$

   where t is the generation number. The species state in the next generation is synchronously updated:

$$S_i(t+1) = \begin{cases} 1 & \text{(alive) if } h_i(t) \geq 0 \\ 0 & \text{(extinct) otherwise} \end{cases} \tag{3}$$

   This step allows for the selection and extinction of species.

3. *Diversification*: We colonize vacant sites freed by extinct species with surviving species. Specifically, a colonizer c will be randomly chosen from the set of survivors. For all vacant sites (i.e. those such that $S_k(t) = 0$) the new connections will be updated in this way:

$$\begin{aligned} W_{k,j} &= W_{c,j} + \eta_{k,j} \\ W_{j,k} &= W_{j,c} + \eta_{j,k} \end{aligned} \tag{4}$$

   where η is a small random variation and $S_k(t+1) = 1$.

This model was shown to reproduce most of the statistical features of macroevolution [8, 10] and it provided a natural source for the decoupling between microevolution (i.e. those processes modeled by genetic algorithms involving selection and continuous adaptation) and macroevolution (i.e. those processes involving extinction and diversification)[9]. Because of the essentially different nature of this approximation, we could ask which kind of outcome would be expected from the application of this model to optimization problems. As we will see, the macroevolution model allows to construct a simple but powerful method of optimization which is able to outperform GAs in several relevant examples.

5 Macroevolutionary Algorithm

In this section we show how to map the previous model of extinction into a model of optimization. The new model will be called a *macroevolutionary algorithm* (MA). Let us define the d-dimensional fitness function f as a multidimensional function that we want to maximize. Our objective is to find the best values for the d-dimensional vectors of our problem under consideration. Thus our individuals/species are now $S_i \equiv \mathbf{p} \in \Omega \in \Re^d$, i.e. d-dimensional objects constrained to a subspace Ω. In this context $\mathbf{p}$ will be a good approximation if $\forall \mathbf{q} : f(\mathbf{q}) \leq f(\mathbf{p}) + \epsilon$ where $\mathbf{p}$ and $\mathbf{q}$ are individuals and $\epsilon > 0$ is a given error threshold.

In this way each individual in MA is described by a d-input vector with fitness f. The domains for these inputs describe the search space where our fitness function is nothing but a (more or less) rugged landscape.

As with GA, MA uses a constant population size of P individuals evolving in time by successive updates of the given operators. The main idea is that our system will choose, through network interactions, which are the individuals to be eliminated so as to guarantee exploration by new individuals and exploitation of better solutions by further generations. To this purpose, it is essential to correctly establish a relationship between individuals. This is described by the following criteria:
(a) Each individual gathers information about the rest of the population through the strength and sign of its couplings W_{ij}. Individuals with higher inputs h_i will be favoured. Additionally, they must be able to outcompete other less-fit solutions.
(b) Some information concerning how close two solutions are in Ω is required (although this particular aspect is not strictly necessary). Close neighbors will typically share similar f-values and will cooperate. In this context, we can define the connection $W_{i,j}$ as:

$$W_{i,j} = \frac{f(\mathbf{p}_i) - f(\mathbf{p}_j)}{\mid \mathbf{p}_i - \mathbf{p}_j \mid} \tag{5}$$

where $\mathbf{p}_i = (p_i^1, ..., p_i^d)$ are the input parameters of the i-th individual. The numerator is a consequence of our first criterion, while the second criterion is introduced in the denominator as a normalization factor that weights the relative distance among solutions.

Now we can define the most important ingredients that will be used in building the set of operators to be applied each generation:

1. *Selection operator*: It allows to calculate the surviving individuals through their relations, i.e. as a sum of penalties and benefits. The state of a given individual S_i will be given by:

$$S_i(t+1) = \begin{cases} 1 & \text{if } \sum_{j=1}^{P} W_{i,j}(t) \geq 0 \\ 0 & \text{otherwise} \end{cases} \tag{6}$$

where t is generation number and $W_{i,j} = W(\mathbf{p}_i, \mathbf{p}_j)$ is calculated according to equation (5). In the following this rule will be indicated as $S_i(t+1) = \theta(h_i(t))$ where $\theta(z) = 1$ if $z \geq 0$ and zero otherwise. Additionally, if the distance D_{ij} between two solutions is zero then we set $W_{ij}(D_ij = 0)$.

2. *Colonization operator*: It allows to fill vacant sites freed by extinct individuals (that is, those such that $S_i = 0$). This operator is applied to each extinct individual in two ways. With a probability τ, a totally new solution $\mathbf{p}_n \in \Omega$ will be generated. Otherwise exploitation of surviving solutions takes place through colonization. For a given extinct solution $\mathbf{p}_i$, we choose one of the surviving solutions, say $\mathbf{p}_b$. Now the extinct solution will be "attracted" towards $\mathbf{p}_b$.

   Mathematically, a possible (but not unique) choice for this colonization of extinct solutions reads:

$$\mathbf{p}_i(t+1) = \begin{cases} \mathbf{p}_b(t) + \rho\lambda(\mathbf{p}_b(t) - \mathbf{p}_i(t)) & \text{if } \xi > \tau \\ \mathbf{p}_n & \text{if } \xi \leq \tau \end{cases} \tag{7}$$

   where $\xi \in [0,1]$ is a random number, $\lambda \in [-1,+1]$ (both with uniform distribution) and ρ and τ are given constants of our algorithm. So we can see that ρ describes a maximum radius around surviving solutions and τ acts as a temperature.

Although all essential rules defining the MA have been presented, several improvements and additional rules have been explored. In particular, we can decrease τ with time as in simulated annealing[4, 7, 11] to get a good convergence. In this context, the "temperature" τ, when lowered, provides a decrease in randomness which favours the exploitation around the best individual found. In order to lower τ in each generation, we can use a given decreasing function. Here we have used a linear relation:

$$\tau(t; G) = 1 - \frac{t}{G} \quad . \tag{8}$$

where G is number of generations. The results of using this linear annealing procedure do not strongly differ from other choices of $\tau(t)$.

6 Mean-field theory

In this section we will introduce a qualitative approximation to the basic MA behavior, which is based on a competition process among the largest peaks, eventually followed by a symmetry-breaking phenomenon when the peaks are very similar.

To make our argument clear, let us assume the simplest case with two peaks with fitness f_k^*, f_r^*, located at two given points $\mathbf{p}_k$ and $\mathbf{p}_r$. For simplicity we will assume that $0 \le f_k^*, f_r^* \le 1$. A given number of solutions will be clustered around these peaks. Let us call Γ_k and Γ_r the sets of solutions around each peak, i.e. we will assume that if $\mathbf{p}_a, \mathbf{p}_b \in \Gamma_k$, then $f(\mathbf{p}_a) \approx f(\mathbf{p}_b) \approx f_k^*$. Let D_{rk} the distance between peaks, and let us assume that $f_k^* - f_r^* = \eta \ge 0$. Let $N^k(t)$ and $N^r(t)$ the number of solutions at each peak at a given step t.

The two operators act on each population around each peak. We can describe the time evolution of our system in terms of two steps:

$$N^k(t+1) = \mathcal{D}_{\rho,\tau}\left[\mathcal{E}_{W_{ij}}(N^k(t))\right] \tag{9}$$

where $\mathcal{E}$ and $\mathcal{D}$ indicate extinction and diversification operators, respectively. Let us first introduce the extinction step. For the Γ_k population we have:

$$N^k(t+1/2) = \mathcal{E}_{W_{ij}}(N^k(t)) = \sum_{i\in\Gamma_k} \theta(G_\mu(\mathbf{p}_i, \mathbf{p}_j)) \tag{10}$$

where we use the notation $G_\mu(\mathbf{p}_i, \mathbf{p}_j)) \equiv \sum_j^P W_{ij}$. So the final expression for the Γ_k population is:

$$N^k(t+1/2) = \sum_{i\in\Gamma_k} \theta\left[\sum_{j\in\Gamma_k} \frac{\epsilon^k}{\delta(\rho)} + \sum_{j\in\Gamma_r} G_\mu(\mathbf{p}_i, \mathbf{p}_j)\right] \tag{11}$$

And an equivalent expression can be derived for the second peak:

$$N^r(t+1/2) = \sum_{i\in\Gamma_r} \theta\left[\sum_{j\in\Gamma_r} \frac{\epsilon^k}{\delta(\rho)} + \sum_{j\in\Gamma_k} G_\mu(\mathbf{p}_i, \mathbf{p}_j)\right] \tag{12}$$

where both populations have been explicitly separated. In our approximation, we assume that the Γ_k set is formed by a closely related set of solutions, which are close inside a domain of size $\mu(\Gamma_k)$ and radius $\delta(\rho)$. This radius clearly depends in some simple way on rule (2). Here we just assume that δ is small (after the clustering process). There are two terms in the previous equation which involve interactions among solutions in the same cluster and interactions among solutions of both clusters. We can assume that the first term is small compared with the cross-interaction term. This approximation will of course depend of the specific properties

of the landscape but is reasonable in terms of our previous assumptions. Here we also assume that the number of random solutions generated by rule (2) (which will depend on τ) is small and so we can approximate $N^k + N^r \approx P$.

A mean-field set of equations (i.e. a first approximation ignoring correlations) can be derived from the previous approximation for the extinction operator. The basic equation for N^k is:

$$N^k(t+1/2) = N_t^k\left(1 - P[\theta(z) < 0]\right) \tag{13}$$

and an equivalent expression for $N^r(t+1/2)$. Now we can use the following (mean field) approximation:

$$\left\langle \theta(G_\mu(\mathbf{p}_i, \mathbf{p}_j)) \right\rangle_{\Gamma_z} \approx \frac{N^z(t)}{D_{rk}} g_z(\eta) \tag{14}$$

where $z \equiv k, r$. The function $g_z(\eta)$ involves the specific response of each population to the difference in fitness between peaks and $D_{r,k}$ stands for the distance among maxima.

The following pair of nonlinear discrete maps is obtained:

$$N^k(t+1/2) = N^k(t)\left[1 - g_k(\eta)\frac{N^r(t)}{PD_{rk}}\right] \tag{15}$$

$$N^r(t+1/2) = N^r(t)\left[1 - g_r(\eta)\frac{N^k(t)}{PD_{rk}}\right] \tag{16}$$

Let us note that, strictly speaking, an additional equation for the $N^n(t)$-population (the one formed by randomly generated solutions) should also be included. Here we assume that it is very small and typically formed by low-fit individuals. The functions $g_z(\eta)$ must fulfil some basic requirements. Several choices are possible (and all of them lead to the same basic results). The simplest is: $g_k(\eta) = \eta(f_k^* - \eta)$ and $g_r(\eta) = \eta f_k^*$. The first g_k-function tells us that the Γ_r-population will have a negative effect on Γ_k proportionally to its fitness but also to the difference between peaks. As this difference increases, it is less likely for the smaller peak to have some harmful effect on Γ_k. For simplicity, since all the dynamics depends on the *difference* between peaks, we will use $f_k^* = 1$.

The next step in our analysis involves diversification. Following our previous approximations, it is not difficult to show that the equations for this second step read:

$$N^k(t+1) = N^k(t+1/2) + \Psi_k(P - N^k(t+1/2) - N^r(t+1/2)) \tag{17}$$

$$N^r(t+1) = N^r(t+1/2) + \Psi_r(P - N^k(t+1/2) - N^r(t+1/2)) \qquad (18)$$

where the coefficients Ψ_z involve both the colonization of Ω by the survivors towards the Γ_k domain, as well as the generation of new, random solutions. It is not difficult (although tedious) to show that these coefficients are: $\Psi_k = \eta(1-\tau) + \xi_k\tau$ $\Psi_r = \eta(1-\eta)(1-\tau) + \xi_r\tau$. The second term in this quantities indicate the likelihood that a random solution falls into one of the Γ sets. Explicitly, $\xi_z \equiv \mu(\Gamma_z)/\mu(\Omega)$, where $\mu(z)$ is the measure (i.e. hypervolume) of each set.

After some algebra, using equations (15-18) and the continuous approximation $N^z(t+1) - N^z(t) \approx dN^k/dt$, the full equations for the MA mean field dynamics are obtained:

$$\frac{dN^k}{dt} = \Psi_k(P - N^r) + N^k\Big(\Psi_k(\beta(2-\eta)N^r - 1) - \beta(1-\eta)N^r\Big) \qquad (19)$$

$$\frac{dN^r}{dt} = \Psi_r(P - N^k) + N^r\Big(\Psi_r(\beta(2-\eta)N^k - 1) - \beta(1-\eta)N^k\Big) \qquad (20)$$

where $\beta = \eta/PD_{rk}$.

This dynamical system can be studied in terms of standard stability analysis [1]. It can be easily shown that the only fixed points here are $(P,0)$ and $(0,P)$. It is worth mentioning that our model involves a competition process which is different from a standard Lotka-Volterra (LV) model of two-species competition [6]. The LV model is defined by two nonlinear differential equations $dx/dt = \mu_1 y(P-x-\beta_1 y)$ and $dy/dt = \mu_2 y(P-y-\beta_2 x)$, where x, y are the population sizes, μ is the growth rate of each one and $\beta_i > 0$ the competition coefficients. The LV model also involves the two so-called exclusion points $(P,0)$ and $(0,P)$ but also two additional ones, $(0,0)$ and $(x^* > 0, y^* > 0)$. The last one implies that coexistence among competitors can take place for some parameter combinations. In the model (19-20) no such coexistence can take place. This is important, as far as for optimization purposes no coexistence among different peaks is desired.

The Jacobi matrix $J_{ij} = (\partial N^i/\partial N^j)$ for our model can be computed for the two fixed points and the eigenvalues are such that, for $\eta > 0$, $\lambda_\pm(P,0) < 0$ and $\lambda_\pm(0,P) > 0$, so a stable and an unstable node are associated to $(P,0)$ and $(0,P)$ respectively. In fact it can be shown that $(P,0)$ is globally stable, attracting all initial conditions towards Γ_r (figure 1).

A particular case is given by η=0, where the same fitness is obtained for each peak. In terms of optimization, this is not a major problem, since we want to find the best solution. The vector field for this case is also shown in Figure 2, where we can see that the trajectories converge to a full line given by $N^r = P - N^k$. This is

what we could expect if we introduce $\eta = 0$ in the previous equations. This leads to a linear system of equations

$$\frac{dN^k}{dt} = \xi_k \tau (P - N^r - N^k) \tag{21}$$

$$\frac{dN^r}{dt} = \xi_r \tau (P - N^r - N^k) \tag{22}$$

which shows that, for the two-cluster problem with $N^n = 0$, the dynamics settles in a final state where a fraction of the population clusters around one peak and the other around the second. Numerical evidence shows, however, that this is not the case: symmetry-breaking (i.e. the choice among one of the two equal peaks) typically occurs: small fluctuations and the presence of random solutions eventually shifts the system towards one of the two peaks.

7 Numerical Results

A number of numerical experiments have been performed in order to study the behavior of MAs and their superiority in relation with standard genetic algorithms. Several functions have been used to this purpose, and are listed below[1].

(1) Two 2-input (i.e. two-dimensional) functions (see Figure 1) of the form

$$f(\vec{x}) = \sum_{i=1}^{m} \frac{a_i e^{\alpha_i}}{e^{\|\vec{x} - P(i)\|^2}} \tag{23}$$

The two specific examples are:

(a) A landscape f_1 with some local maxima of close heights where $m = 10$ and $\vec{x} \in [0, 100]^2$ (see Fig. 3) The location of the maxima is given in the following table:

$\vec{P}_i$	(35,85)	(75,75)	(25,30)	(45,45)	(80,55)
	(65,55)	(25,65)	(85,15)	(90,90)	(70,10)
a_i	40	55	75	99	85
	95	85	65	92	35
α_i	35	30	45	55	60
	20	70	40	40	55

(b) A landscape f_2 with infinite maxima around the global maximum where $m = 2$ and $\vec{x} \in [0, 100]^2$ (figure 3.)

[1] For all the numerical experiments, a Sun Ultra-1 workstation with SunOS operating system has been used for all the numerical experiments.

$\vec{P}_i$	(50,50)	(50,50)	(50,50)
a_i	750	-720	35
α_i	500	425	25

(2) In order to obtain a standard comparison with previous studies, we have also used several multivalued functions proposed in the contest held during the 1996 IEEE International Conference on Evolutionary Computation for real valued spaces containing five N-input functions:
(c) The sphere model where $x_i \in [-5, 5]$ with $N = 10$:

$$f_3(\vec{x}) = -\sum_{i=1}^{N}(x_i - 1)^2 \tag{24}$$

(d) Griewank's function where $x_i \in [-600, 600]$ with $N = 10$:

$$f_4(\vec{x}) = -\frac{1}{4000}\sum_{i=1}^{N}(x_i - 100)^2 + \prod_{i=1}^{N}\cos\left(\frac{x_i - 100}{\sqrt{i}}\right) + 1 \tag{25}$$

(e) Shekel's foxholes where $x_i \in [0, 10]$ with $N = 10$:

$$f_5(\vec{x}) = \sum_{i=1}^{N}\frac{1}{\|\vec{x} - A(i)\|^2 + c_i} \tag{26}$$

(f) Langerman's function where $x_i \in [0, 10]$ with $N = 10$:

$$f_6(\vec{x}) = \sum_{i=1}^{N} c_i e^{\frac{1}{\pi}\|\vec{x} - A(i)\|^2}\cos(\pi\|\vec{x} - A(i)\|^2) \tag{27}$$

(g) Michalewicz's function where $x_i \in [0, \pi]$ with $N = 10$:

$$f_7(\vec{x}) = \sum_{i=1}^{N}\sin(x_i)\sin^{20}\left(\frac{ix_i^2}{\pi}\right) \tag{28}$$

(h) Rotated Michalewicz's function version where $x_i \in [0, \pi]$ with $N = 10$ and $\alpha = \frac{\pi}{4}$:

$$f_8(\vec{x}) = f_7(Rotation(\vec{x}))$$

where *Rotation* means to perform $N - 1$ rotations of α radians centered at point $(\frac{\pi}{2}, {}^{(n}\ldots, \frac{\pi}{2})$.

As a first approximation to numerically explore MA's behavior, we have represented (as points on the Ω domain) scores of local maxima and the population distribution at four different time steps for the two-input functions f_1 and f_2 (see FIGS.

2 and 3). The role of randomness is shown graphically with this 2D-representation: Initially, MA explores the input space looking for good individuals, which are clustered around local maxima (in the figures, stage with $t = 10$). Afterward (see the plot at $t = 30$ and $t = 45$) *competition* between maxima takes place by attracting more individuals/solutions. Finally, at stage $t = 70$, it is expected that the global maximum wins because it captures all individuals.

In order to understand how the two parameters ρ and τ influence MA behavior, three types of experiments were performed for f_1 and f_2 using equal population sizes for both functions ($P = 50$) over $G = 400$ generations and for $R = 50$ independent runs. Explicitly, we considered the following situations: (a) ρ is varied using values in $[0, 1]$, while τ is fixed; (b) ρ is varied using values in $[0, 1]$, and τ is varied using linear simulated annealing according to the equation (8) and (c) τ is varied using values $[0, 1]$, while ρ is fixed. In order to quantify the differences, the following measures were used: (1) Mean of best fitness value reached; (2) Mean number of generations needed in order to reach a good fitness value (98.0199 for f_1, and 64.3500 for f_2) and (3) Probability of success in reaching a good fitness value f^*, measured as the relative number of runs that have reached f^*.

The basic results of these experiments are summarized in Figure 4. We can see that there is no well-defined optimum for neither τ nor ρ. Typically a wide range of parameter values gives similar results. These results allow us to reduce the number of parameters which should be tuned in our algorithm to just two: population size P and number of generations G to be calculated.

Actually, in most cases simulated annealing seems to be the best choice, being the specific ρ-value less important. For this reason, MA with linear simulated annealing will be used in our study. In all our simulations we will use $\rho = 0.5$. In FIG. 5, we compare MA with and without simulated annealing by measuring the mean fitness for all solutions in the population in each generation: for MA with simulated annealing (i.e. with reduced exploration in favour of exploitation) the mean tends monotonically to the optimum, while for τ constant, the population shows lower fitness values, close to GA results.

To further simplify the comparison between MA and GA, standard values of $p_c = 0.7$ and $p_m = 0.001$ for the genetic algorithm will be used (other reasonable choices gave equivalent statistical results). In the GA model, individuals are represented by a 32-bit sequence. Moreover, due to the fact that GA shows premature convergence for some functions, another selection operator, tournament selection [5] (choosing the best of two random individuals with a probability of, say, 0.75) will be used.

A first comparison between GA and MA —with and without simulated annealing— is shown in FIG. 6 where single runs using the three methods are plotted. Here FIGS. 6A, 6B, 6C and FIGS. 6D, 6E, 6F correspond to runs of the first and second examples

of our list, respectively. These pictures shows that, while MA converges progressively with time, the GA tends to show considerable fluctuations.

In order to mesure and compare their performance, several extensive simulation experiments were used (see Figure 9) for f_1 and f_2 using different population sizes ($P \in [50, 400]$) over $G = 400$ generations and using $R = 50$ independent runs. The following measures were used:
(a) Mean of best fitness value reached after R runs. (b) Mean number of generations required to reach a good fitness value ($f^* = 98.0199$ for f_1, and $f^* = 64.3500$ for f_2). (c) Probability of reaching a good fitness value. (d) The time used (in clock ticks) to reach a good fitness value.

Many different simulation experiments were performed in order to compare the advantages of MA in relation with GA with tournament selection. The main results and conclusions from our simulations are:

1. Macroevolutionary algorithms reach higher fitness values than GAs for equal population sizes. The difference between both approaches decreases if P is large enough (simply due to fact that MA have already reached the optimum while GA continues exploring).

2. The probability of success in reaching a good fitness value along G generations in a typical run is higher in MA than in GA.

3. The time needed to reach the optimum using the same population size is lower in MA if the population size is small. But for large P (see Figure 9), the time required in each iteration by MA can become larger than for GA (order P^2 vs P).

The asymptotic time difference is due to the *selection operator*, which is computationally more expensive. In standard GA, this operator chooses individuals with a probability proportional to their fitness in a time scale of order $O(P \log P)$, but if tournament selection is used, it is only $O(P)$. In contrast, MA involves a time scale of order $O(P^2)$. For this reason, a comparison of these measures for both algorithms with equal populations P is not adequate. A alternative could be to apply a readjustment factor to P in terms of time cost. However the relevance of small values for P in the performance of MA makes the asymptotic comparison useless. However, if the distance between candidate solutions is removed from the definition of the couplings (5) a considerable increase in MA performance is obtained, although an extensive re-analysis of our results will be required in order to compare the two cases.

A different approximation can be used. We could be interested in faster but less accurate solutions, or in larger fitnesses but slower convergence. A good comparative

criterion should allow us to explore this compromise between fitness values and the time needed to reach them. To this objective, several experiments have been performed —varying P and G for different sample sizes (R)— in which both the fitness of the best solution reached and time required are measured. These measures have been sorted and averaged over time, and the success probability calculated. The basic results of these simulations are summarized in the next table and in in figures 8, 9 and 10

Funct.	Alg.	P	Δ P	G	Δ G	R	time interval
f_1	GA	50 to 400	20	50 to 400	10	15	25
f_1	MA	50 to 250	10	50 to 400	10	15	25
f_2	GA	50 to 400	20	50 to 400	10	15	25
f_2	MA	50 to 250	10	50 to 400	10	15	25
f_3	GA	220 to 480	20	500 to 5000	300	5	600
f_3	MA	20 to 150	20	500 to 1500	300	5	125
f_4	GA	120 to 270	20	300 to 5000	300	5	600
f_4	MA	20 to 240	20	300 to 5000	100	5	400
f_5	GA	150 to 380	20	500 to 6000	300	5	600
f_5	MA	50 to 240	20	800 to 6000	300	5	400
f_6	GA	150 to 380	20	500 to 6000	300	5	2500
f_6	MA	50 to 240	20	800 to 6000	300	5	2000
f_7	GA	150 to 380	20	500 to 6000	300	5	1200
f_7	MA	50 to 210	20	800 to 6000	300	5	1500
f_8	GA	150 to 380	20	500 to 6000	300	5	2000
f_8	MA	50 to 210	20	800 to 6000	300	5	2000

These experiments shows that, for all the used test functions used —except Michalewicz's function f_7— the MA reaches better fitness values and has a higher success probability the GA. Michalewicz's function f_7 is a particular case where the geometric properties of the landscape favours GA. (However, a simple geometric transformation, like rotations of the function that keep the landscape shape, can strongly modify the GA performance).

8 Conclusions

In this paper we have introduced a novel optimization technique which we have called macroevolutionary algorithm. It is based in a simple procedure inspired in macroevolutionary responses of complex ecosystems to extinction events. In the original model, extinctions removed some species and new ones were generated by

diversification of the survivors. In the MA approach, the basic ecology-like structure is also preserved, but it is now applied to a set of candidate solutions to a given optimization problem on a fitness landscape. The survival of species/solutions is linked with the relative fitness as given by $f(\mathbf{x})$ in relation with all the other species. These differences define the strength of their couplings, weighted by their mutual distance in search space Ω. If the total sum of input connections to a given species is positive, it survives. If negative, it disappears from the system. In this sense, the number of removed solutions is not fixed (as it happen to be the case for standard GA) but strongly dynamical. Sometimes, a large (mass-) extinction event takes place when a very good solution is found. The replacement process guarantees both the exploitation of the high-fit solutions as well as further, random exploration of other domains of the landscape. Because of the connection matrix, the whole population is able to obtain a rather accurate map of the relative importance of the solutions being explored in the landscape.

There are two types of situations to be considered according to whether or not simulated annealing is used. The first case is appropiate when we want to find a good solution in a given number of generations and also guarantee that such a solution is a local optimum within a given confidence. In this case, we should use the linear annealing to increase the exploitation over the last generations. In this way we guarantee that mass extinction will occur when all individuals have reached local optimum. In the second case, when a constant value for τ is used, we keep the same exploration rate along time. This could be interesting when fitness is a time-varying function.

Moreover, other changes have been considered in the algorithm with no qualitative differences: (a) The colonizer b can be chosen by the colonization operator with proportional fitness probability, instead of using just the best individual. Furthermore, we can add the possibility for each extinct individual to choose its own colonizer; (b) To use a different probability distribution (instead of the uniform one) to generate λ in (7).

Numerical simulations have shown that MA typically outperformed GA over a wide range of conditions. Together with a typically monotonous convergence, the interactions between individuals in MA (through the connection matrix $W_{i,j}$) make exploration in input space much more satisfactory. Moreover, MA is being succesfully applied to optimization problems that can be formulated in terms of an optimization function even if it is highly multi-modal or highly multi-dimensional. For example, MA can be successfully applied to learning in neural networks as a training algorithm and as a multidimensional scaling method. Following this aproach, MA could be applied to combinational optimization problems, although the main difficulty is to express the problem in terms of relations between individuals. Further work should

explore the efficiency of the MA in correlated/uncorrelated landscapes. The mean-field approximation to the simple two-peak problem shows that the best solution is always a global attractor of the dynamics. Due to (i) the antisymmetric nature of the connectivity matrix, (ii) the numerical observation that a peak-to-peak competition process takes place through the evolution and (iii) the monotonous change implicit in the competition dynamics, we conjecture that a general analytic treatment of MAs can be derived.

FIG. 13 discloses a representative computer system 1310 in conjunction with which the embodiments of the present invention may be implemented. Computer system 1310 may be a personal computer, workstation, or a larger system such as a minicomputer. However, one skilled in the art of computer systems will understand that the present invention is not limited to a particular class or model of computer.

As shown in FIG. 13, representative computer system 1310 includes a central processing unit (CPU) 1312, a memory unit 1314, one or more storage devices 1316, an input device 1318, an output device 1320, and communication interface 1322. A system bus 1324 is provided for communications between these elements. Computer system 1310 may additionally function through use of an operating system such as Windows, DOS, or UNIX. However, one skilled in the art of computer systems will understand that the present invention is not limited to a particular configuration or operating system.

Storage devices 1316 may illustratively include one or more floppy or hard disk drives, CD-ROMs, DVDs, or tapes. Input device 1318 comprises a keyboard, mouse, microphone, or other similar device. Output device 1320 is a computer monitor or any other known computer output device. Communication interface 1322 may be a modem, a network interface, or other connection to external electronic devices, such as a serial or parallel port

While the above invention has been described with reference to certain preferred embodiments, the scope of the present invention is not limited to these embodiments. One skill in the art may find variations of these preferred embodiments which, nevertheless, fall within the spirit of the present invention, whose scope is defined by the claims set forth below.

Claims

Claims

1. A system for performing optimization on a fitness landscape comprising:

an evolutionary model comprising:

a plurality of species representing a corresponding plurality of candidate solutions to an optimization problem; and

a plurality of rules governing a behavior of said species, said rules comprising:

at least one connectivity rule establishing a plurality of relations among said species;

at least one extinction rule defining an an extinction of said species; and

at least one colonization rule defining a filling of vacancies caused by said extinction; and

a simulator for executing said model to generate one or more optimal solutions to the optimization problem.

2. A system as in claim 1 wherein said at least one connectivity rule randomly chooses connections among said species.

3. A system as in claim 1 wherein said at least one connectivity rule assigns a connectivity value randomly chosen from -1 to 1 to said connections among said species.

4. A system as in claim 3 wherein said extinction rule defines an extinction of each of said species in accordance with said connectivity value.

5. A system as in claim 1 wherein said at least one colonization rule defines said filling of said vacancies by either a new one of said species or an existing one of said species.

6. A system as in claim 5 wherein said at least one colonization rule defines an attraction between a surviving one of said species and an extinct one of said species, said attraction is proportional to a distance between said surviving species and said extinct species.

7. A system as in claim 1 wherein said at least one colonization rule comprises

at least one parameter that influences the filling of vacancies.

8. Computer executable software code stored on a computer readable medium, the code for performing optimization on a fitness landscape, the code comprising:

code to model an optimization problem comprising:

code to represent a plurality of candidate solutions to the optimization problem with a plurality of species; and

code to govern a behavior of said species, said code to govern comprising:

code to establish a plurality of relations among said species;

code to define an extinction of said species; and

code to define a filling of vacancies caused by said extinction; and

code to execute said model to generate one or more optimal solutions to the optimization problem.

9. A programmed computer system for performing optimization as a fitness landscape comprising at least one memory having at least one region storing computer executable program code and at least one processor for executing the program code stored in said memory, wherein the program code comprises:

code to model an optimization problem comprising:

code to represent a plurality of candidate solutions to the optimization problem with a plurality of species; and

code to govern a behavior of said species, said code to govern comprising:

code to establish a plurality of relations among said species;

code to define a survival of said species; and

code to define a filling of vacancies caused by said extinction; and

code to execute said model to generate one or more optimal solutions to the optimization problem.

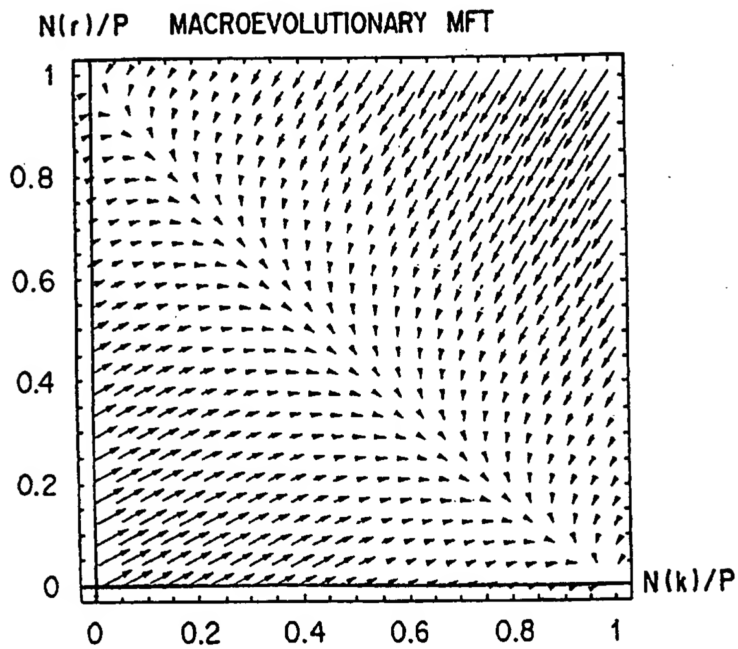


FIG. 1A

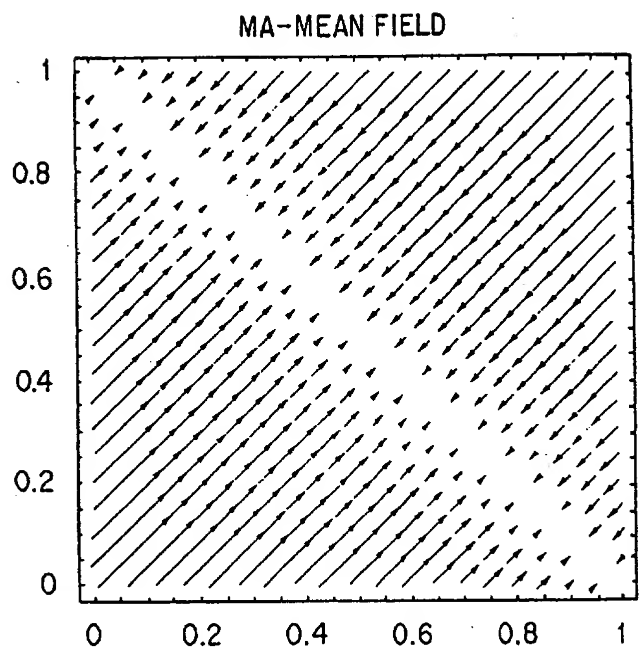
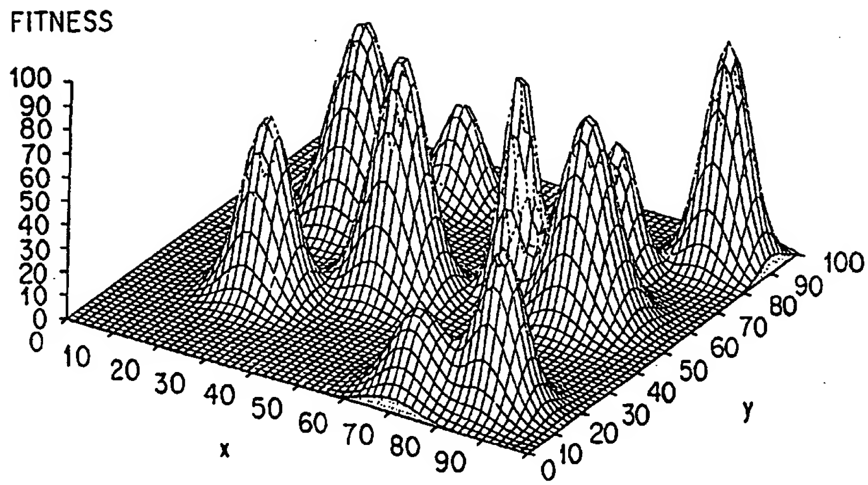


FIG. 1B


FITNESS
100
90
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70
60
50
40
30
20
10
0
0
10
20
30
40
50
60
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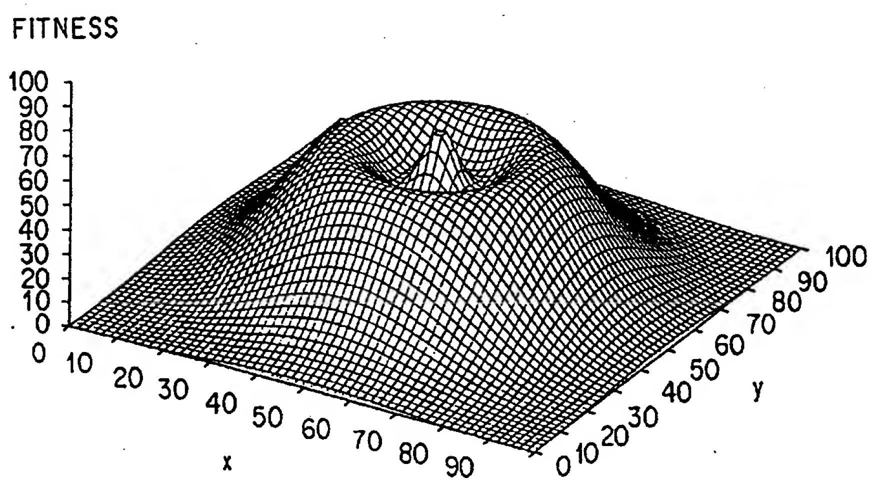
90
x
0
10
20
30
40
50
60
70
80
90
100
y

FIG. 1C


FITNESS
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50
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30
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10
0
0
10
20
30
40
50
60
70
80
90
x
0
10
20
30
40
50
60
70
80
90
100
y

FIG. 1D

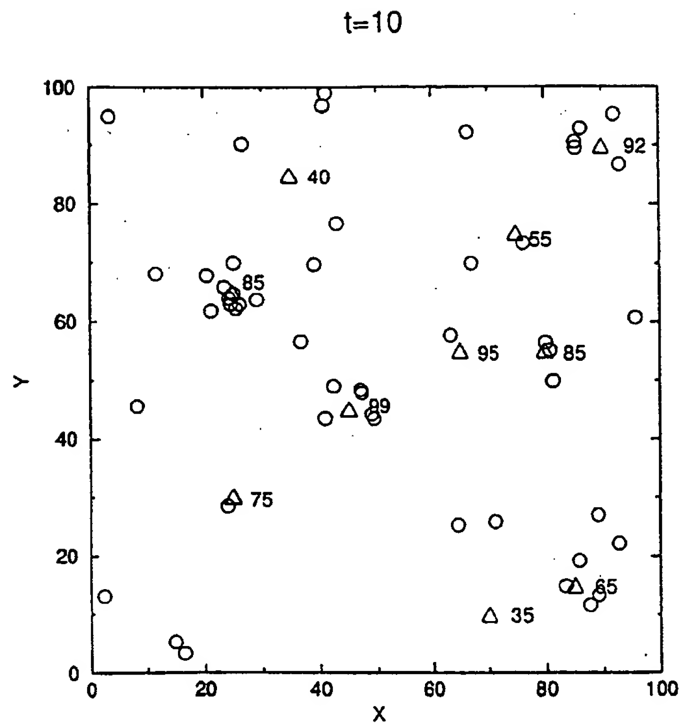


FIG. 2A

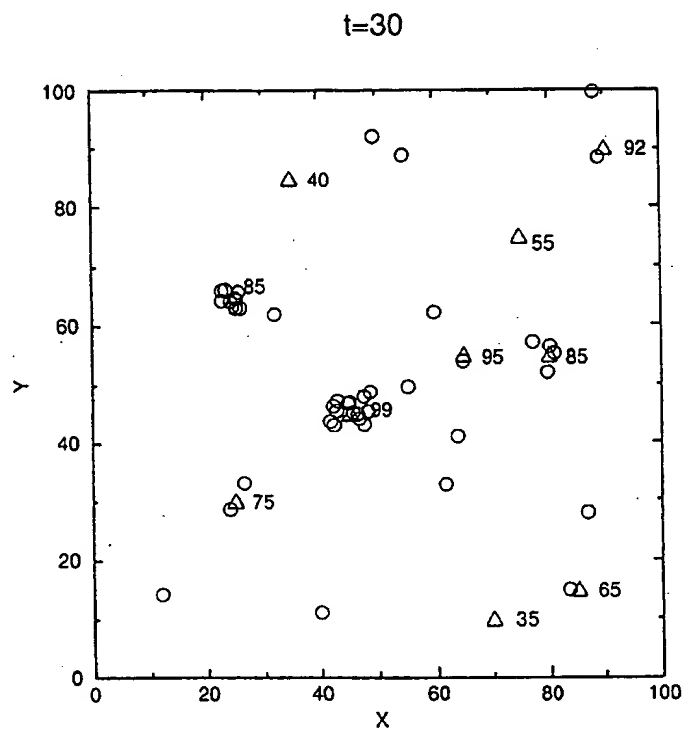


FIG. 2B

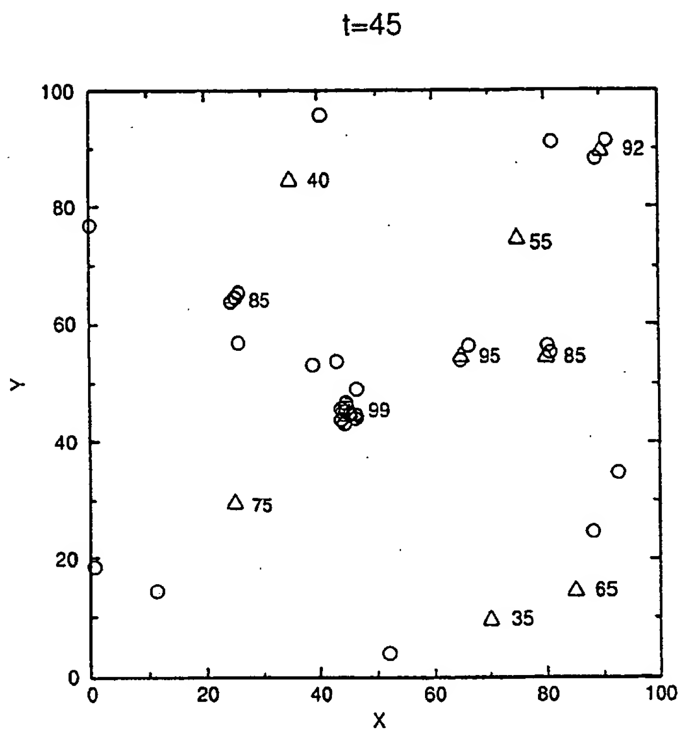


FIG. 2C

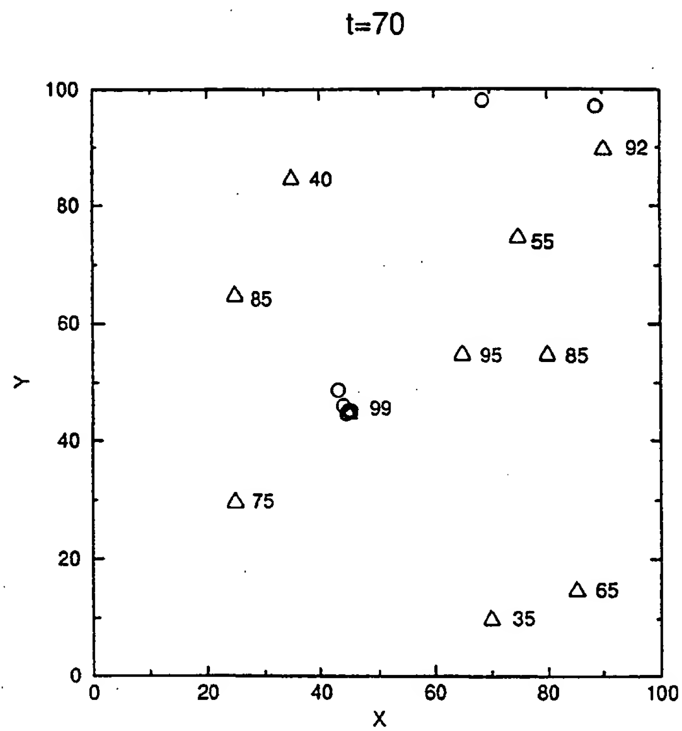


FIG. 2D

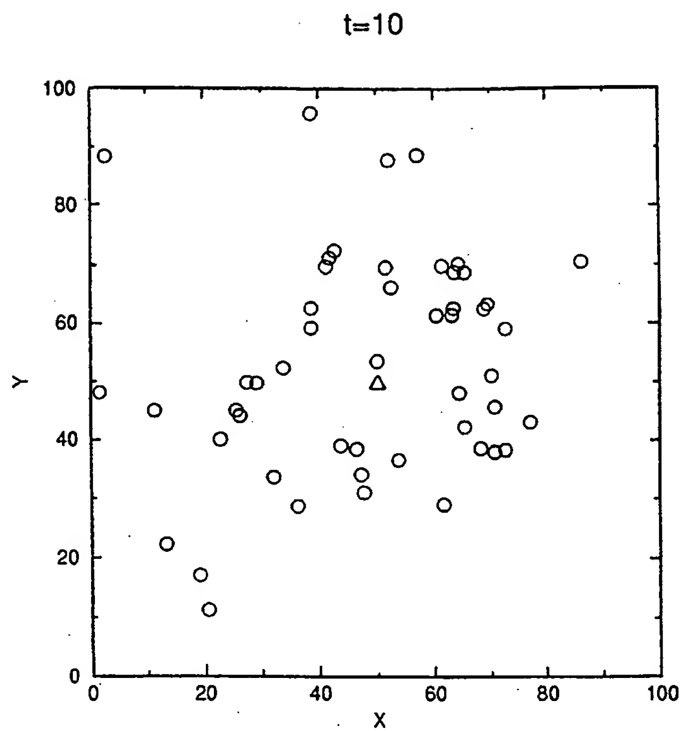


FIG. 3A

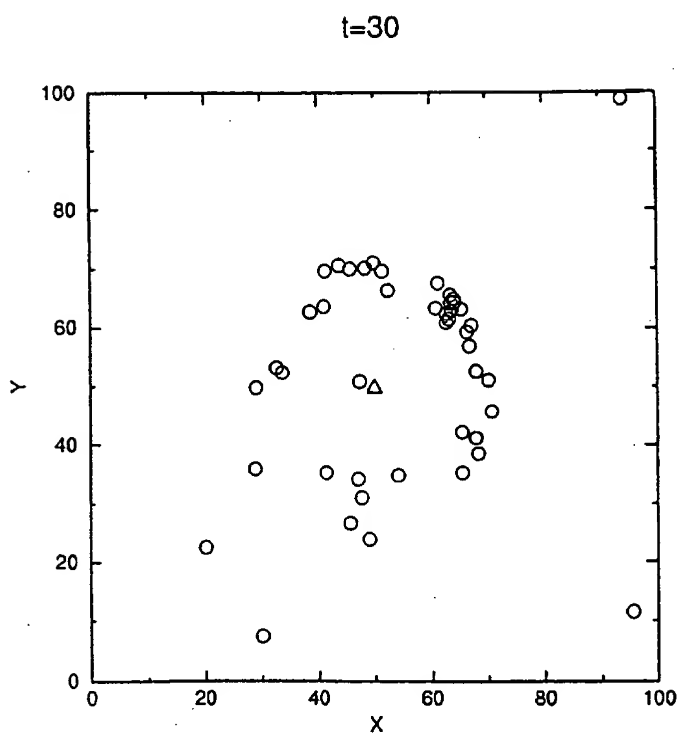


FIG. 3B

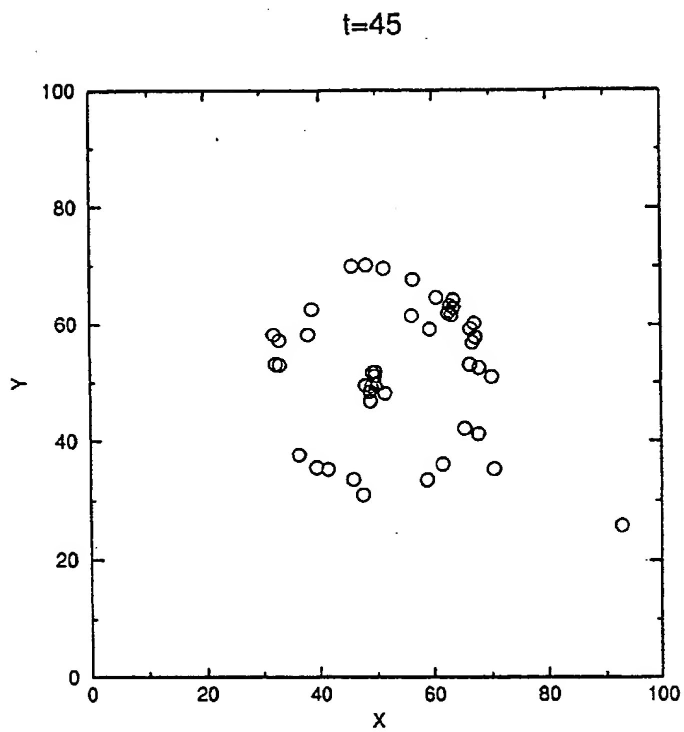


FIG. 3C

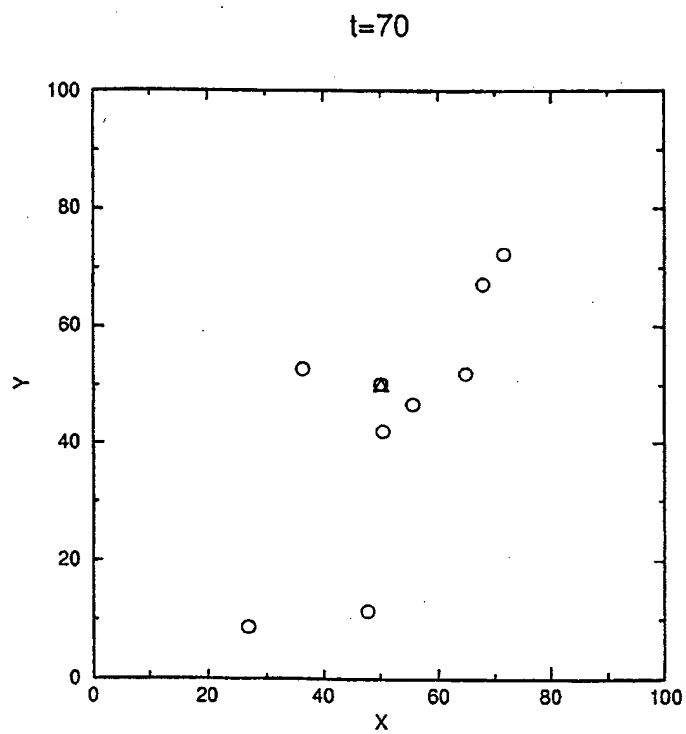
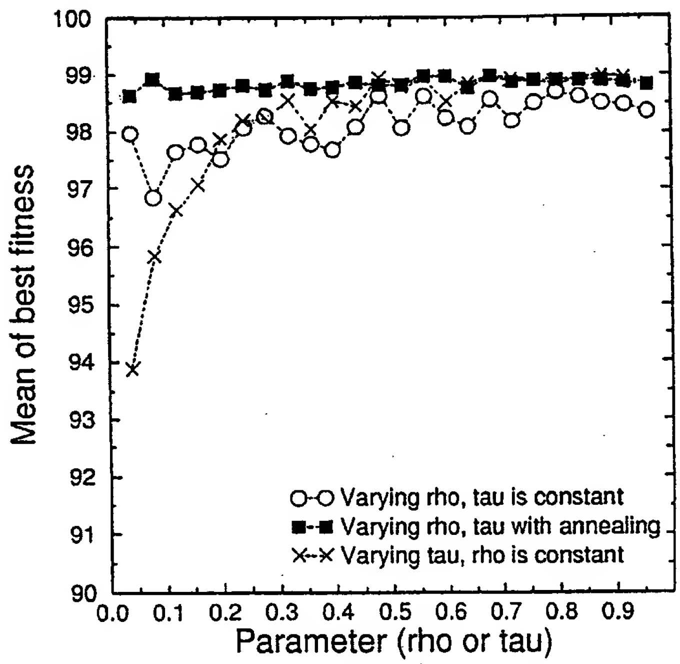
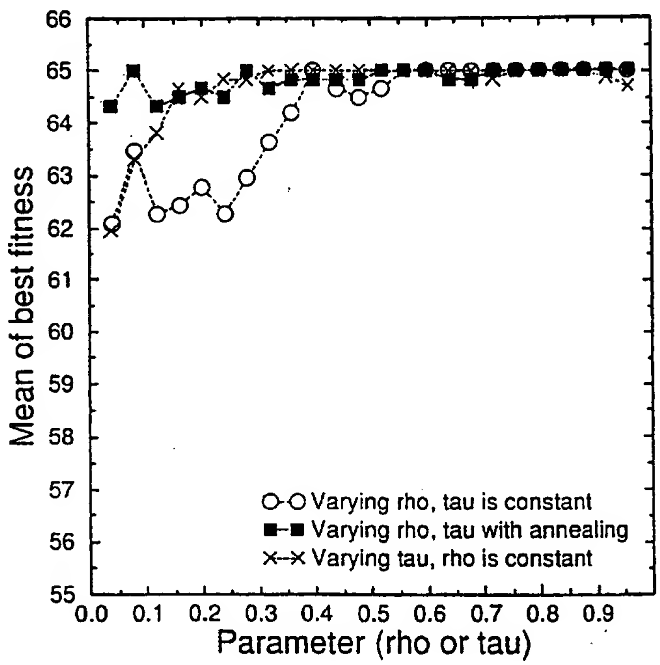


FIG. 3D



100
99
98
97
96
95
94
93
92
91
90
Mean of best fitness
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Parameter (rho or tau)
Varying rho, tau is constant
Varying rho, tau with annealing
Varying tau, rho is constant

FIG. 4A



66
65
64
63
62
61
60
59
58
57
56
55
Mean of best fitness
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Parameter (rho or tau)
Varying rho, tau is constant
Varying rho, tau with annealing
Varying tau, rho is constant

FIG. 4B

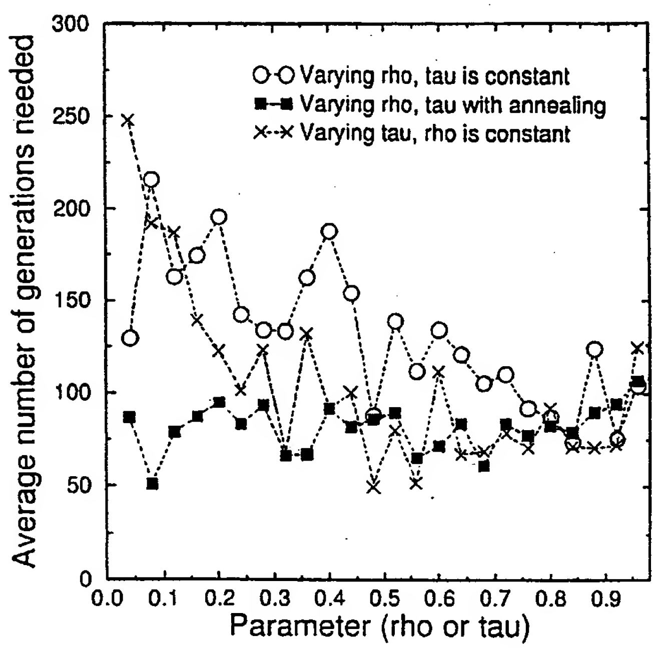
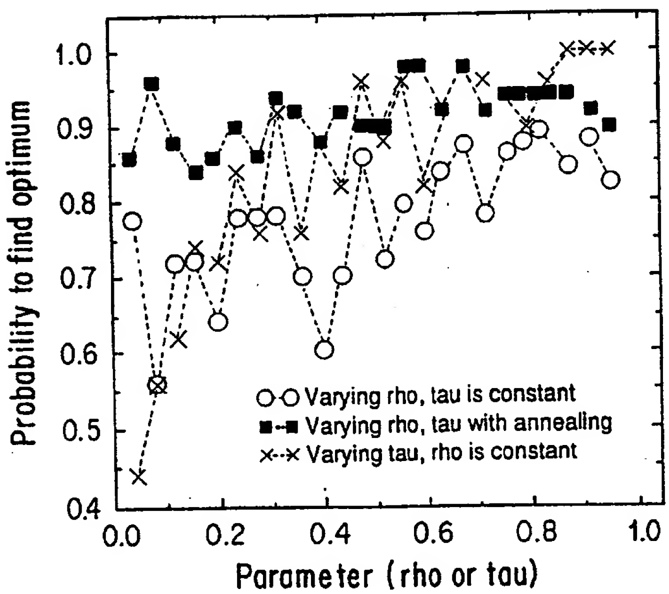

300
250
200
150
100
50
0
Average number of generations needed
O-O Varying rho, tau is constant
■-■ Varying rho, tau with annealing
×-× Varying tau, rho is constant
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Parameter (rho or tau)

FIG. 4C



Probability to find optimum
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.0
0.2
0.4
0.6
0.8
1.0
Parameter (rho or tau)
Varying rho, tau is constant
Varying rho, tau with annealing
Varying tau, rho is constant

FIG. 4D

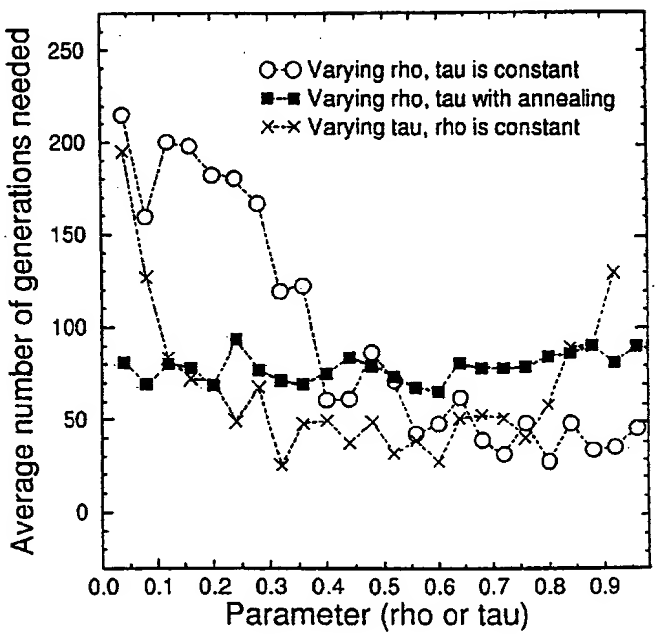

Average number of generations needed
250
200
150
100
50
0
Varying rho, tau is constant
Varying rho, tau with annealing
Varying tau, rho is constant
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Parameter (rho or tau)

FIG. 4E

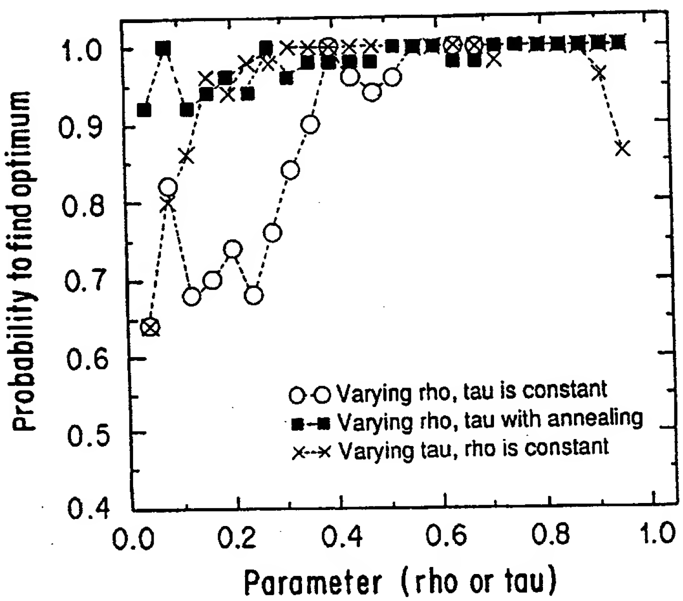
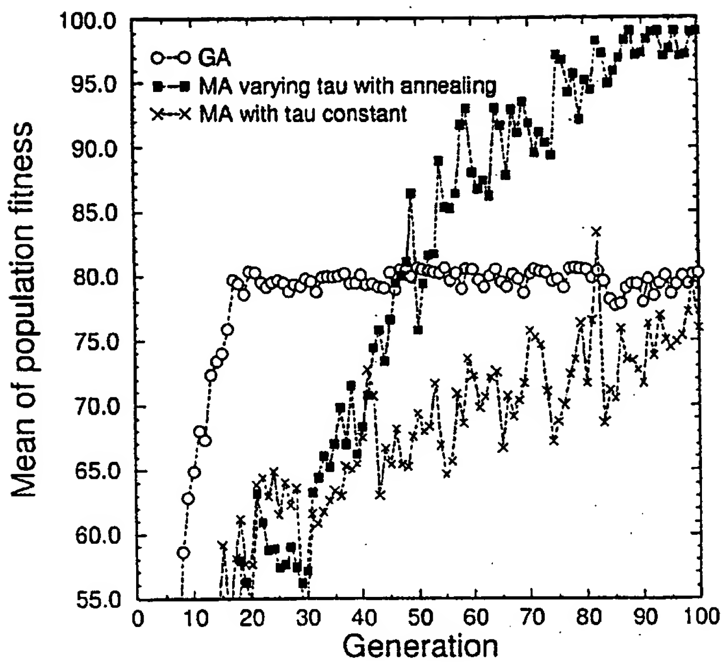
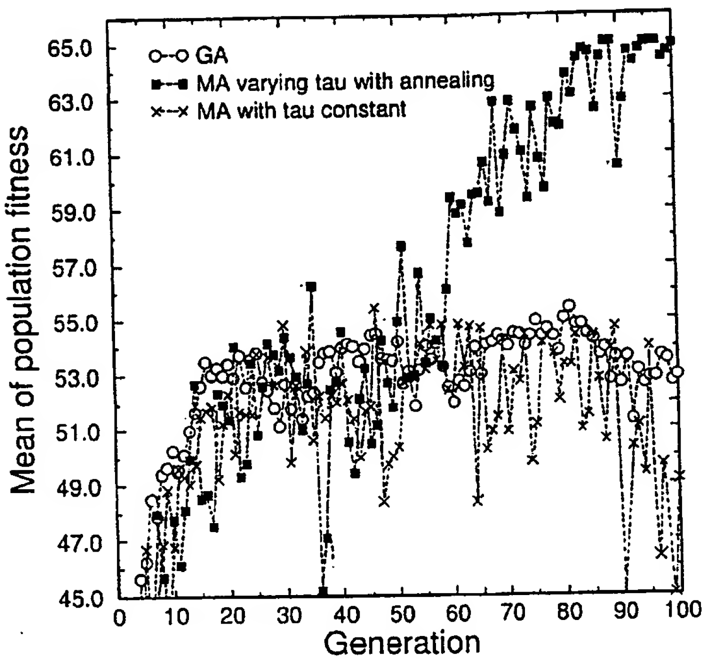

1.0
0.9
0.8
0.7
0.6
0.5
0.4
Probability to find optimum
0.0
0.2
0.4
0.6
0.8
1.0
Parameter (rho or tau)
Varying rho, tau is constant
Varying rho, tau with annealing
Varying tau, rho is constant

FIG. 4F



100.0
95.0
90.0
85.0
80.0
75.0
70.0
65.0
60.0
55.0
Mean of population fitness
GA
MA varying tau with annealing
MA with tau constant
0
10
20
30
40
50
60
70
80
90
100
Generation

FIG. 5A



GA
MA varying tau with annealing
MA with tau constant
Mean of population fitness
65.0
63.0
61.0
59.0
57.0
55.0
53.0
51.0
49.0
47.0
45.0
0
10
20
30
40
50
60
70
80
90
100
Generation

FIG. 5B

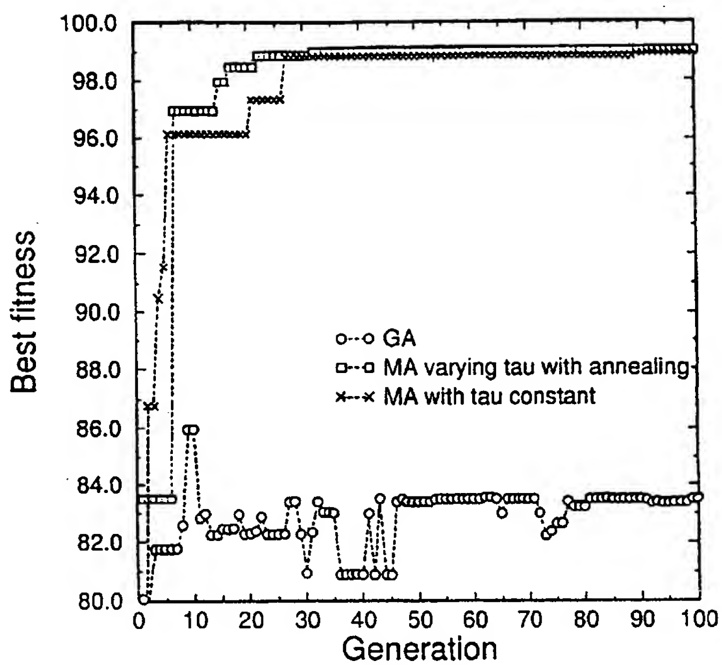
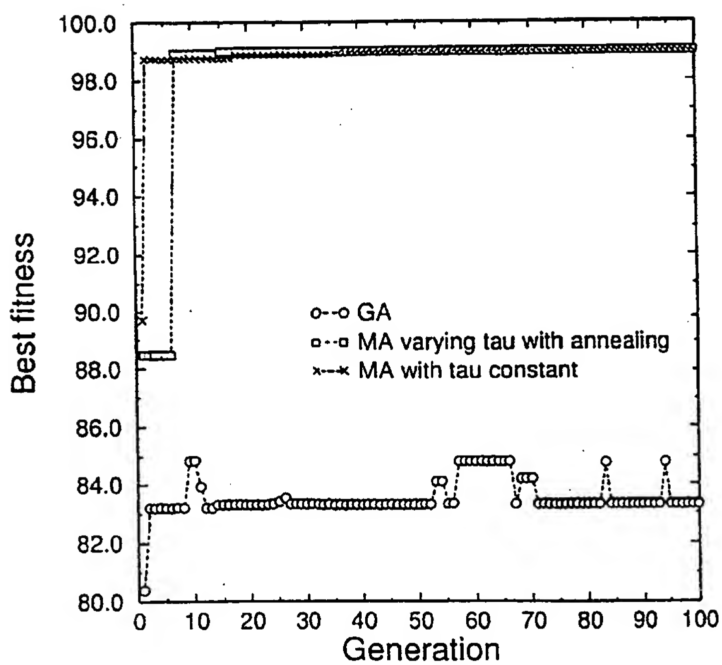

100.0
98.0
96.0
94.0
92.0
90.0
88.0
86.0
84.0
82.0
80.0
Best fitness
0
10
20
30
40
50
60
70
80
90
100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6A



100.0
98.0
96.0
94.0
92.0
90.0
88.0
86.0
84.0
82.0
80.0
Best fitness
0
10
20
30
40
50
60
70
80
90
100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6B

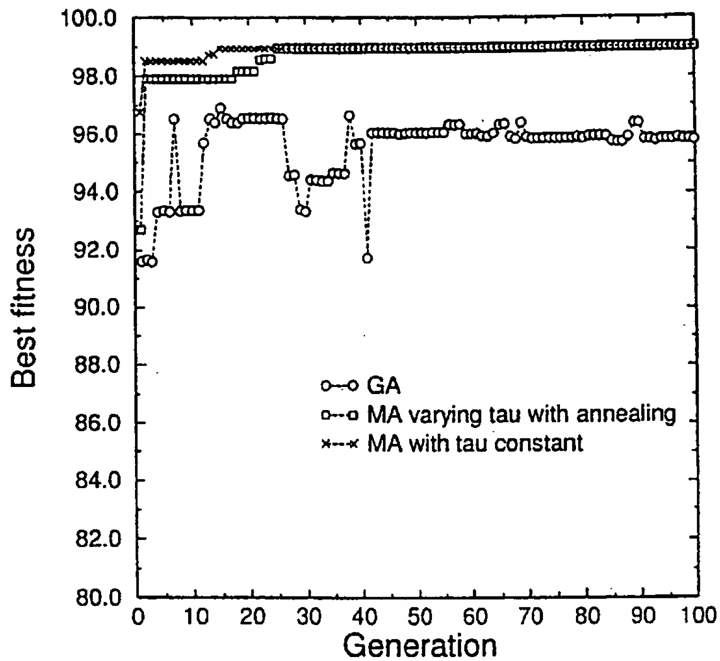
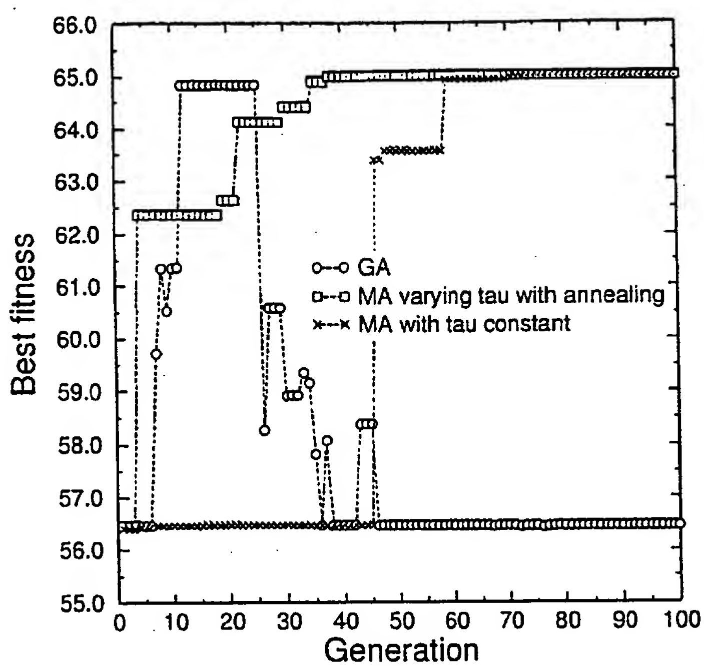

100.0
98.0
96.0
94.0
92.0
90.0
88.0
86.0
84.0
82.0
80.0
Best fitness
0 10 20 30 40 50 60 70 80 90 100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6C



Best fitness
66.0
65.0
64.0
63.0
62.0
61.0
60.0
59.0
58.0
57.0
56.0
55.0
0
10
20
30
40
50
60
70
80
90
100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6D

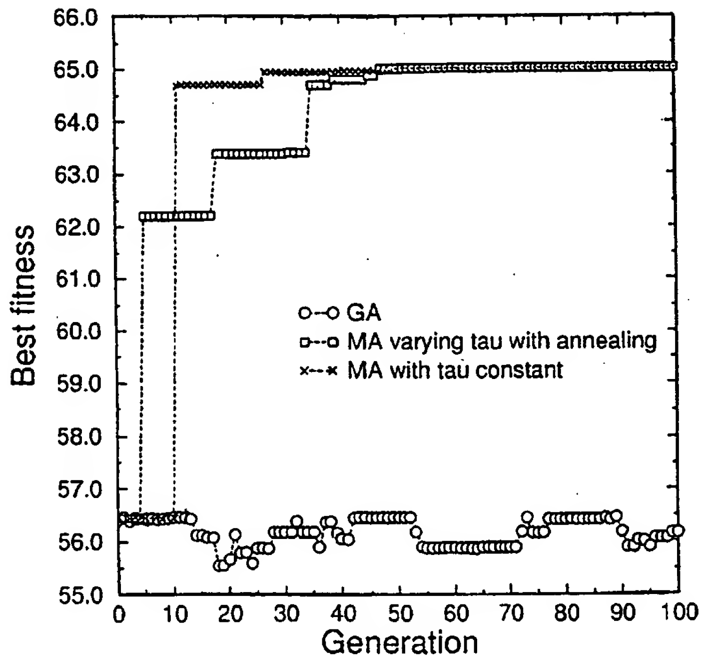

66.0
65.0
64.0
63.0
62.0
61.0
60.0
59.0
58.0
57.0
56.0
55.0
Best fitness
0
10
20
30
40
50
60
70
80
90
100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6E

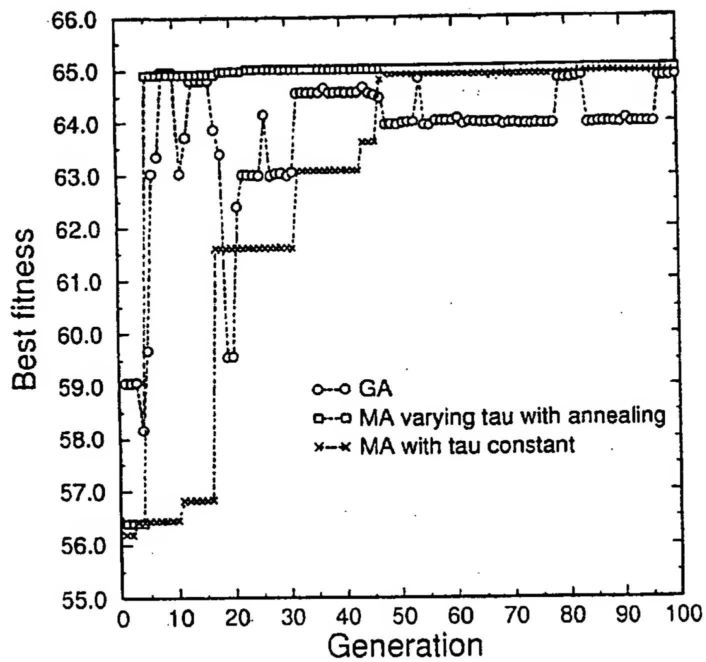
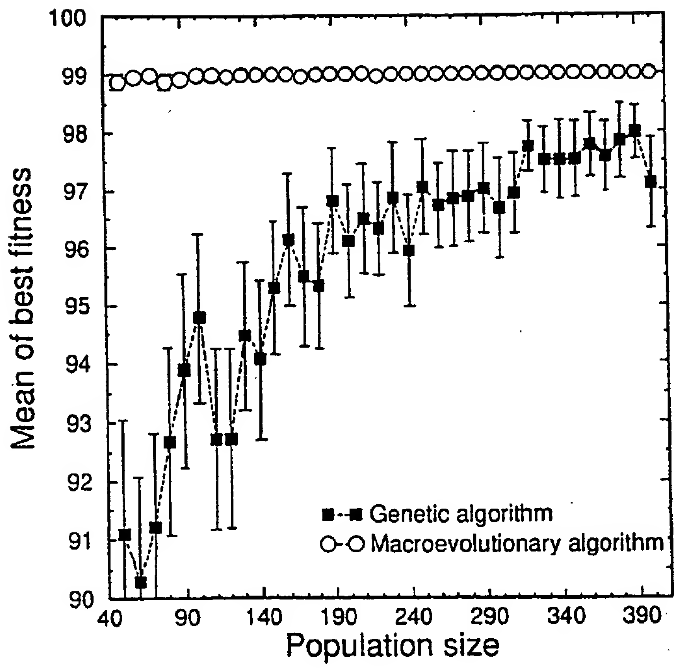

66.0
65.0
64.0
63.0
62.0
61.0
60.0
59.0
58.0
57.0
56.0
55.0
Best fitness
0
10
20
30
40
50
60
70
80
90
100
Generation
GA
MA varying tau with annealing
MA with tau constant

FIG. 6F



Mean of best fitness
100
99
98
97
96
95
94
93
92
91
90
40
90
140
190
240
290
340
390
Population size
Genetic algorithm
Macroevolutionary algorithm

FIG. 7A

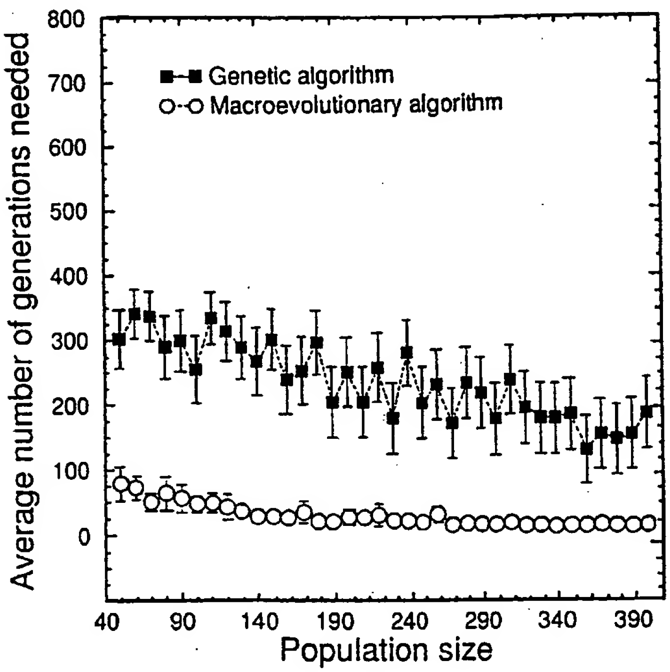
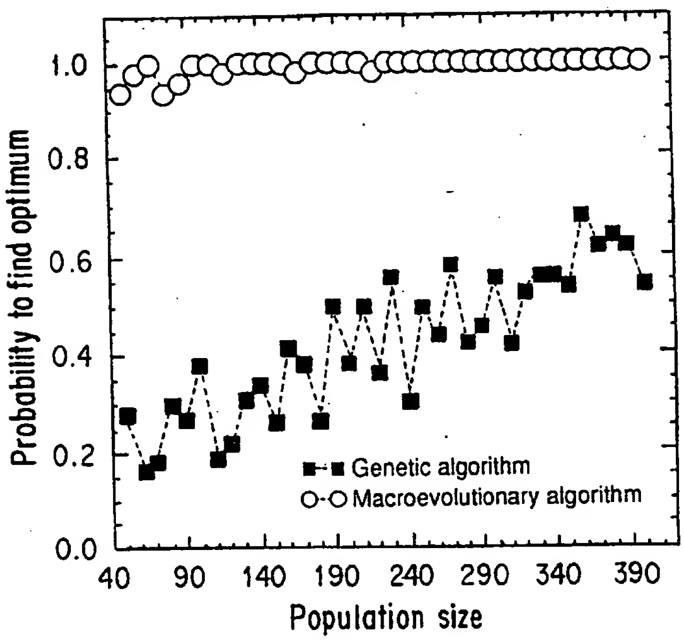
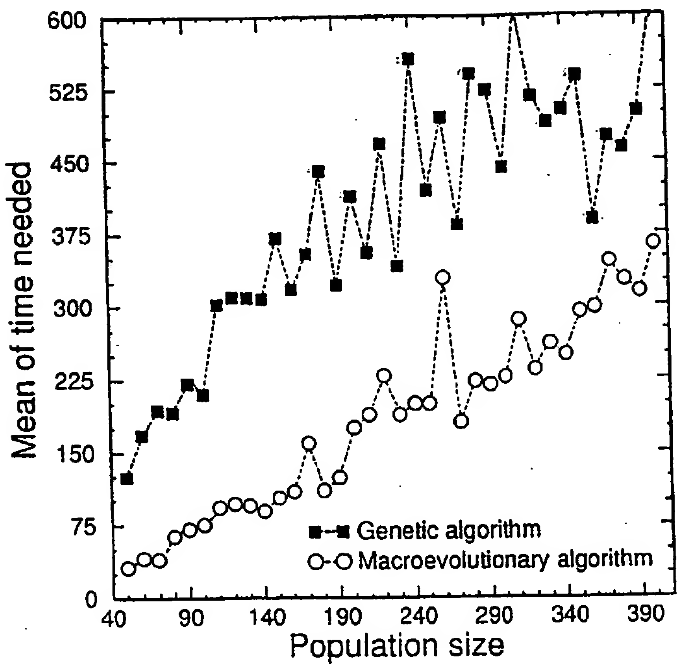

Average number of generations needed
800
700
600
500
400
300
200
100
0
Genetic algorithm
Macroevolutionary algorithm
40
90
140
190
240
290
340
390
Population size

FIG. 7B



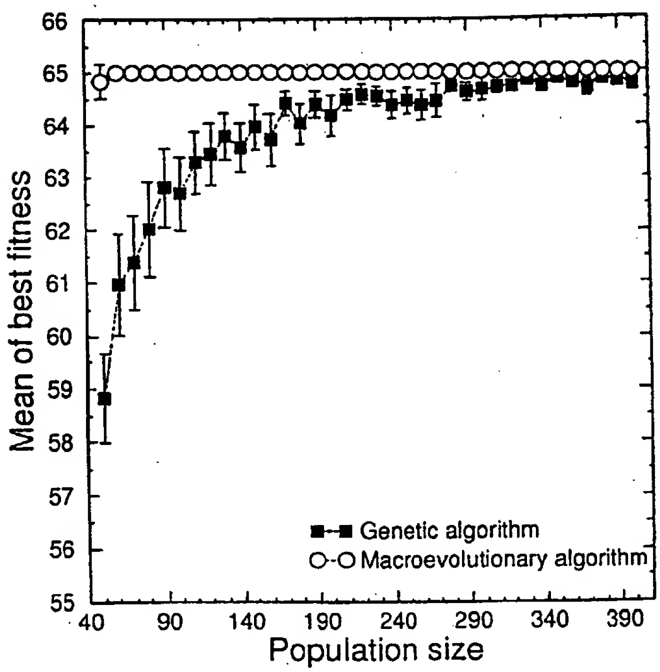
Probability to find optimum
1.0
0.8
0.6
0.4
0.2
0.0
40
90
140
190
240
290
340
390
Population size
Genetic algorithm
Macroevolutionary algorithm

FIG. 7C



600
525
450
375
300
225
150
75
0
Mean of time needed
40
90
140
190
240
290
340
390
Population size
Genetic algorithm
Macroevolutionary algorithm

FIG. 7D



Mean of best fitness
66
65
64
63
62
61
60
59
58
57
56
55
40
90
140
190
240
290
340
390
Population size
Genetic algorithm
Macroevolutionary algorithm

FIG. 7E

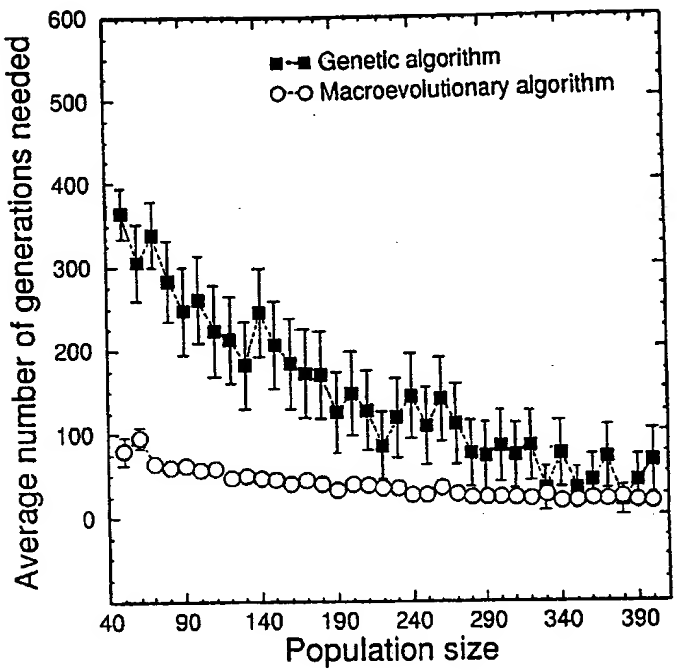
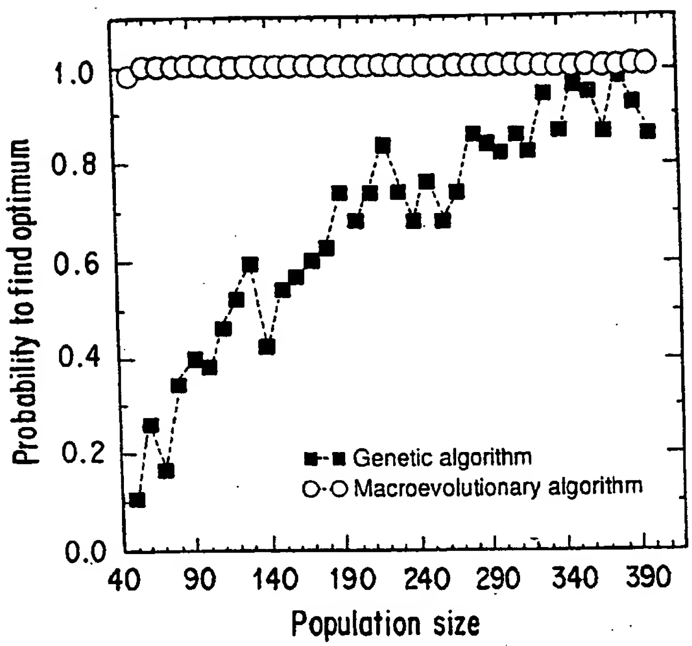

Genetic algorithm
Macroevolutionary algorithm
Average number of generations needed
Population size
600
500
400
300
200
100
0
40
90
140
190
240
290
340
390

FIG. 7F



1.0
0.8
0.6
0.4
0.2
0.0
Probability to find optimum
Genetic algorithm
Macroevolutionary algorithm
40
90
140
190
240
290
340
390
Population size

FIG. 7G

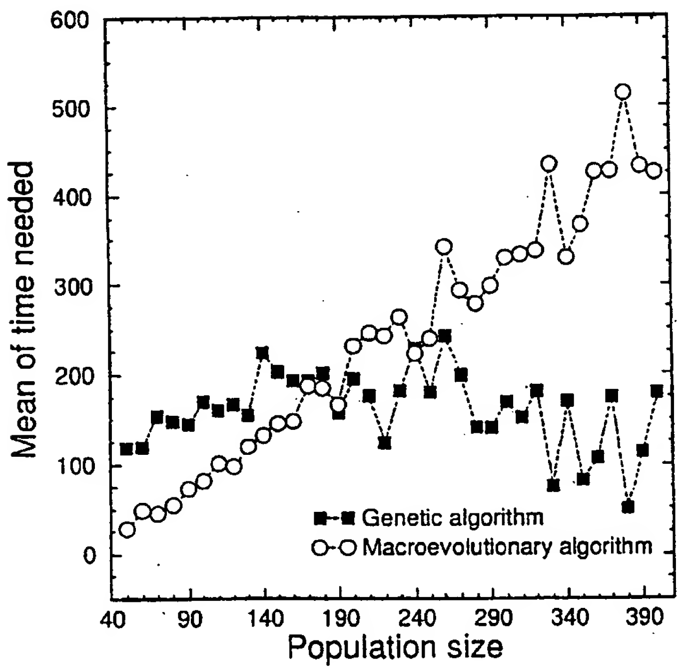
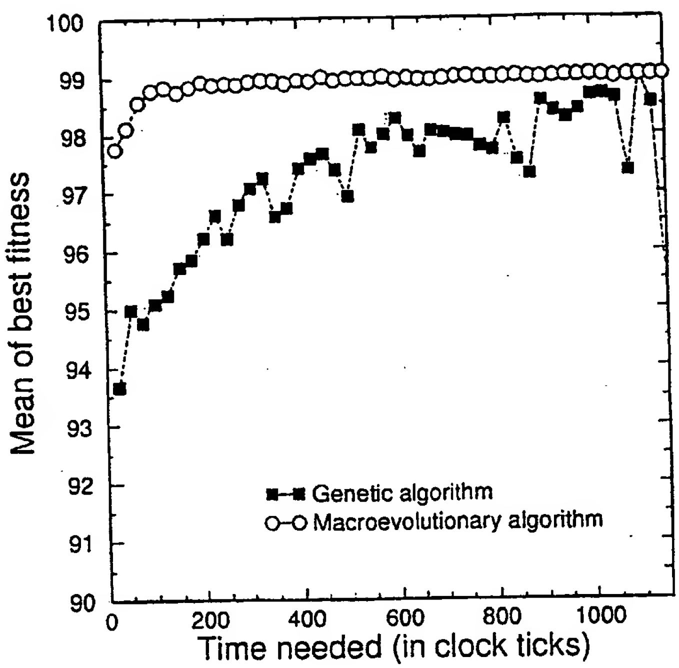

600
500
400
300
200
100
0
Mean of time needed
40
90
140
190
240
290
340
390
Population size
Genetic algorithm
Macroevolutionary algorithm

FIG. 7H



100
99
98
97
96
95
94
93
92
91
90
Mean of best fitness
0
200
400
600
800
1000
Time needed (in clock ticks)
Genetic algorithm
Macroevolutionary algorithm

FIG. 8A

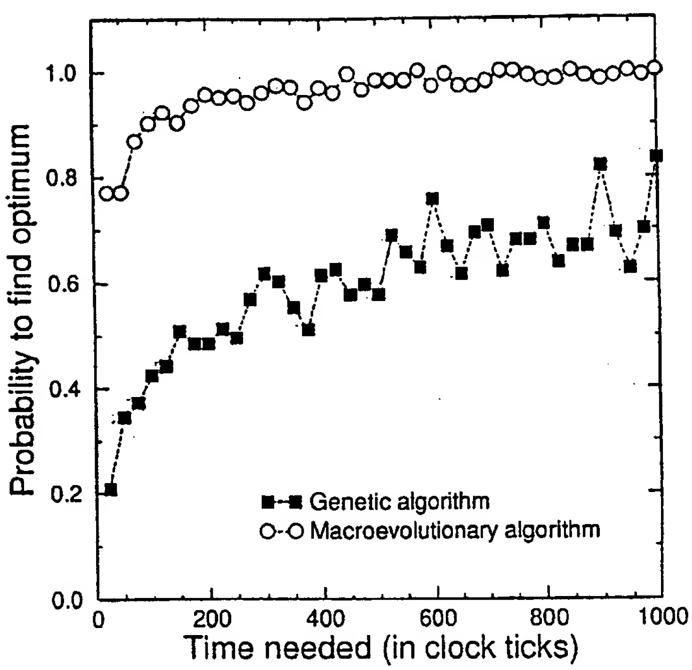
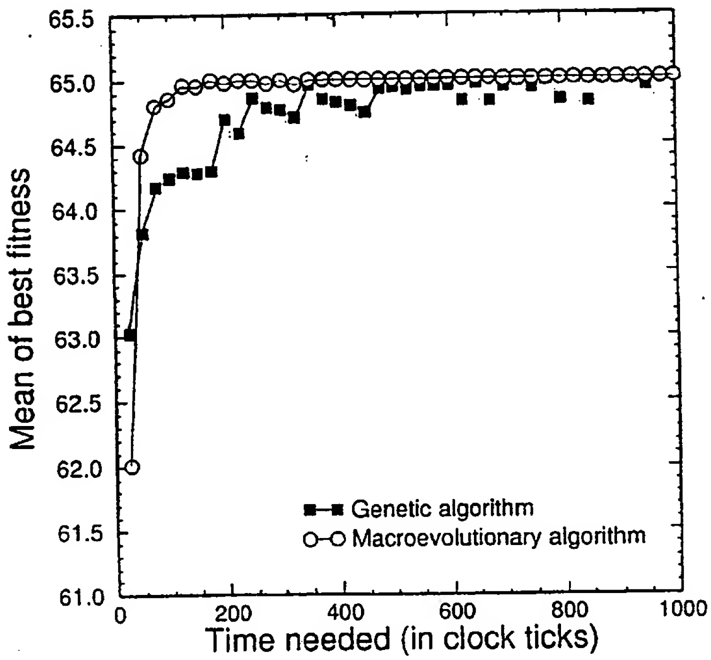
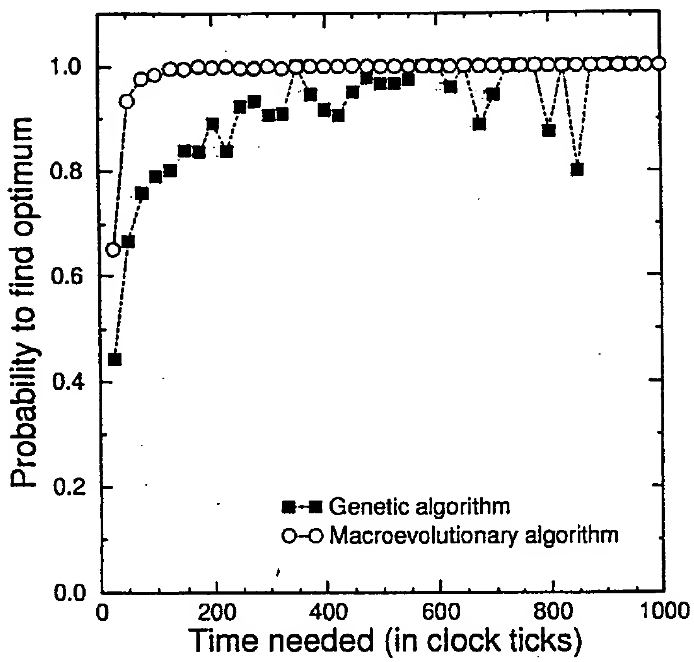

Probability to find optimum
1.0
0.8
0.6
0.4
0.2
0.0
0
200
400
600
800
1000
Time needed (in clock ticks)
Genetic algorithm
Macroevolutionary algorithm

FIG. 8B



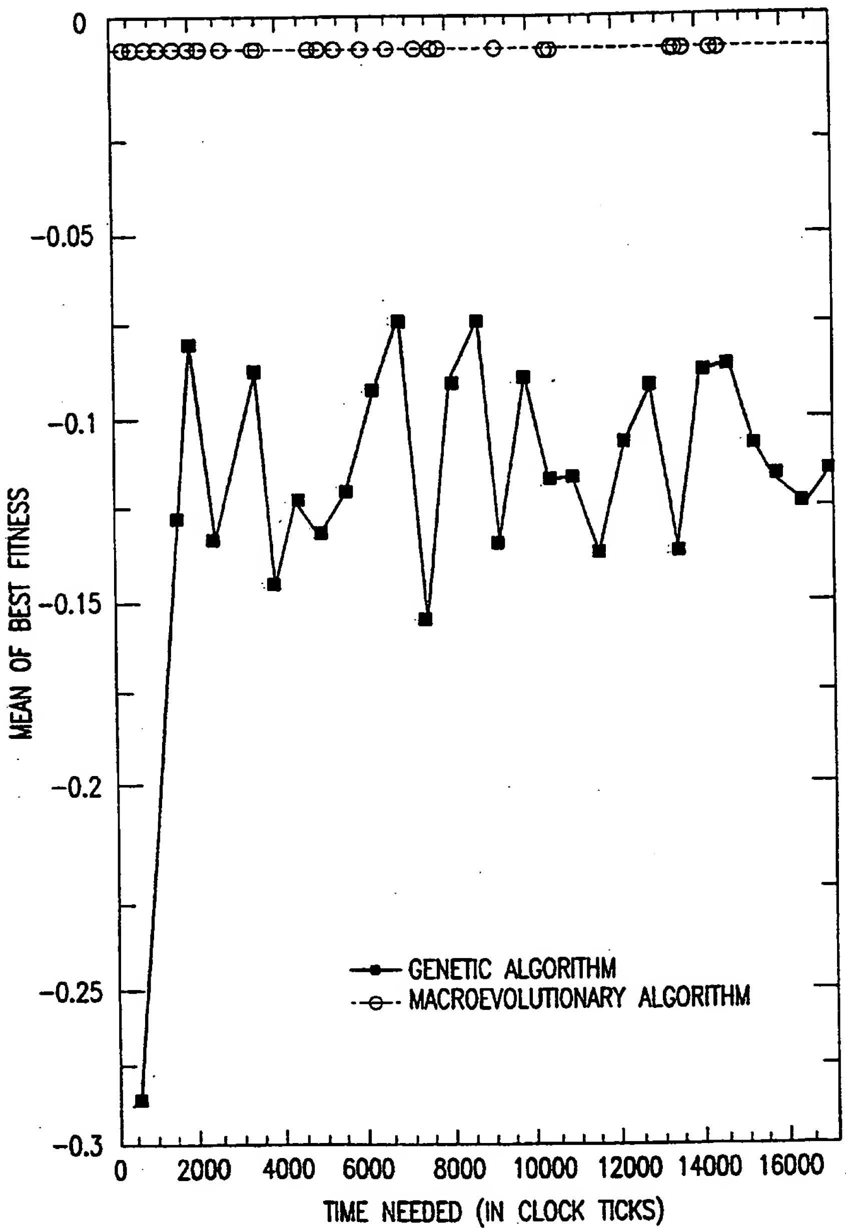
65.5
65.0
64.5
64.0
63.5
63.0
62.5
62.0
61.5
61.0
Mean of best fitness
0
200
400
600
800
1000
Time needed (in clock ticks)
Genetic algorithm
Macroevolutionary algorithm

FIG. 8C



Probability to find optimum
1.0
0.8
0.6
0.4
0.2
0.0
0
200
400
600
800
1000
Time needed (in clock ticks)
Genetic algorithm
Macroevolutionary algorithm

FIG. 8D



0
-0.05
-0.1
-0.15
-0.2
-0.25
-0.3
MEAN OF BEST FITNESS
0 2000 4000 6000 8000 10000 12000 14000 16000
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.9A

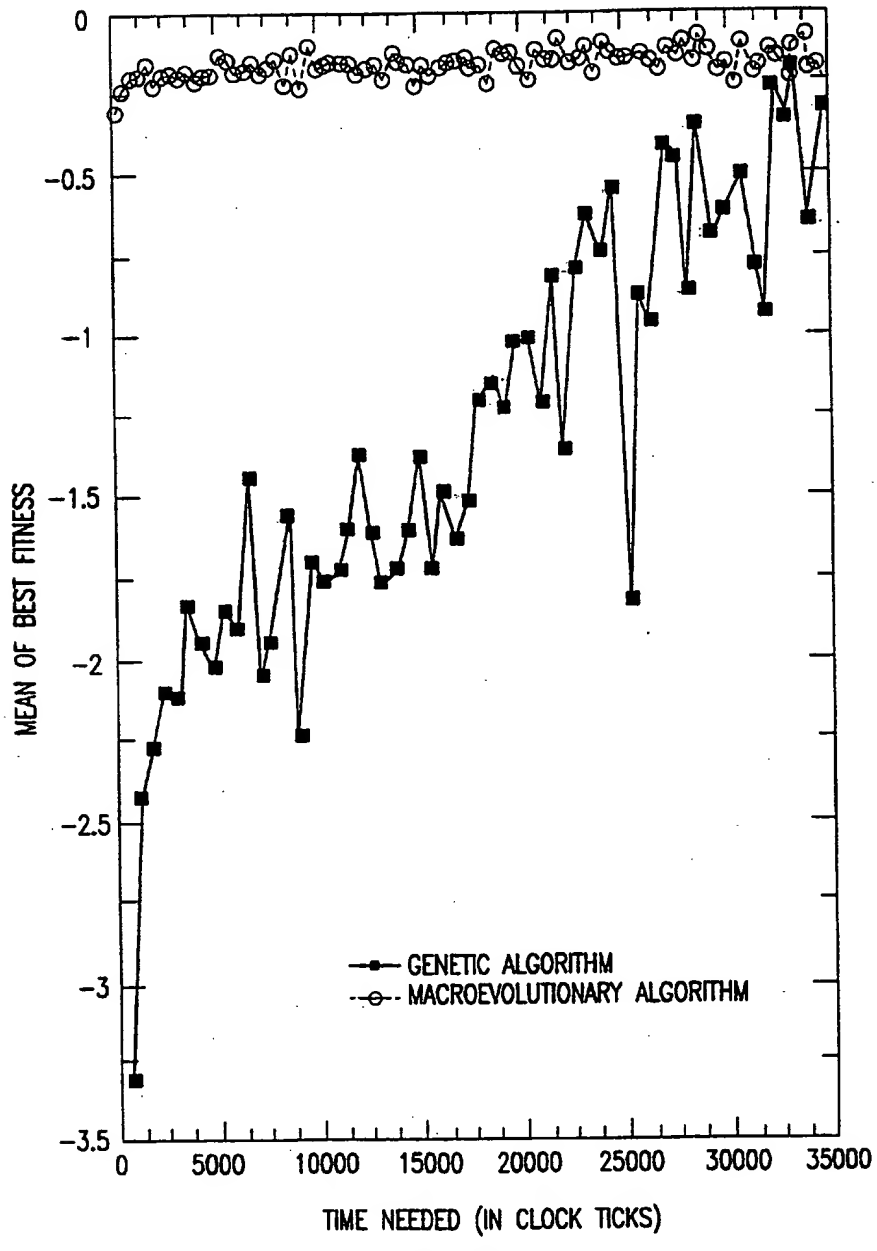

0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
MEAN OF BEST FITNESS
0 5000 10000 15000 20000 25000 30000 35000
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.9B

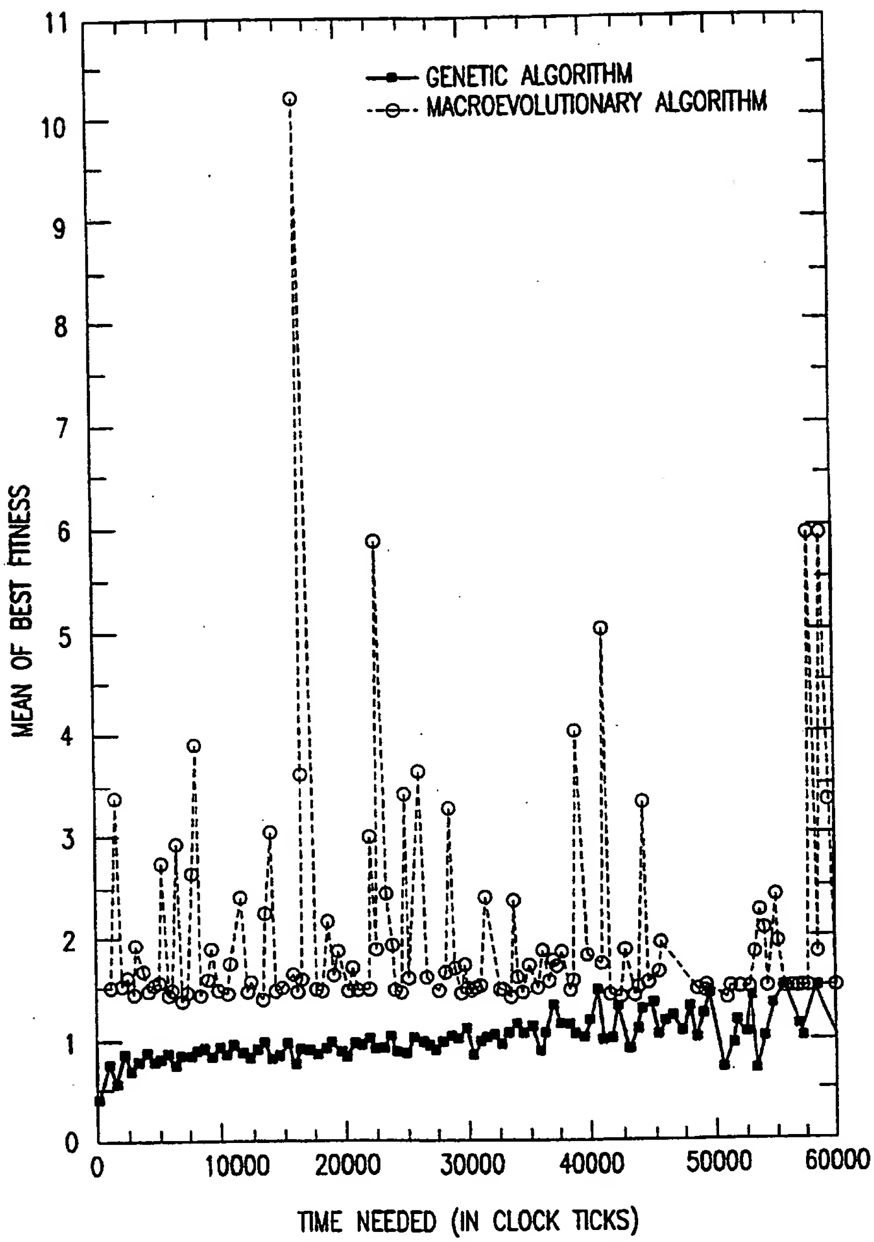

GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
MEAN OF BEST FITNESS
0
1
2
3
4
5
6
7
8
9
10
11
0
10000
20000
30000
40000
50000
60000
TIME NEEDED (IN CLOCK TICKS)

FIG.9C

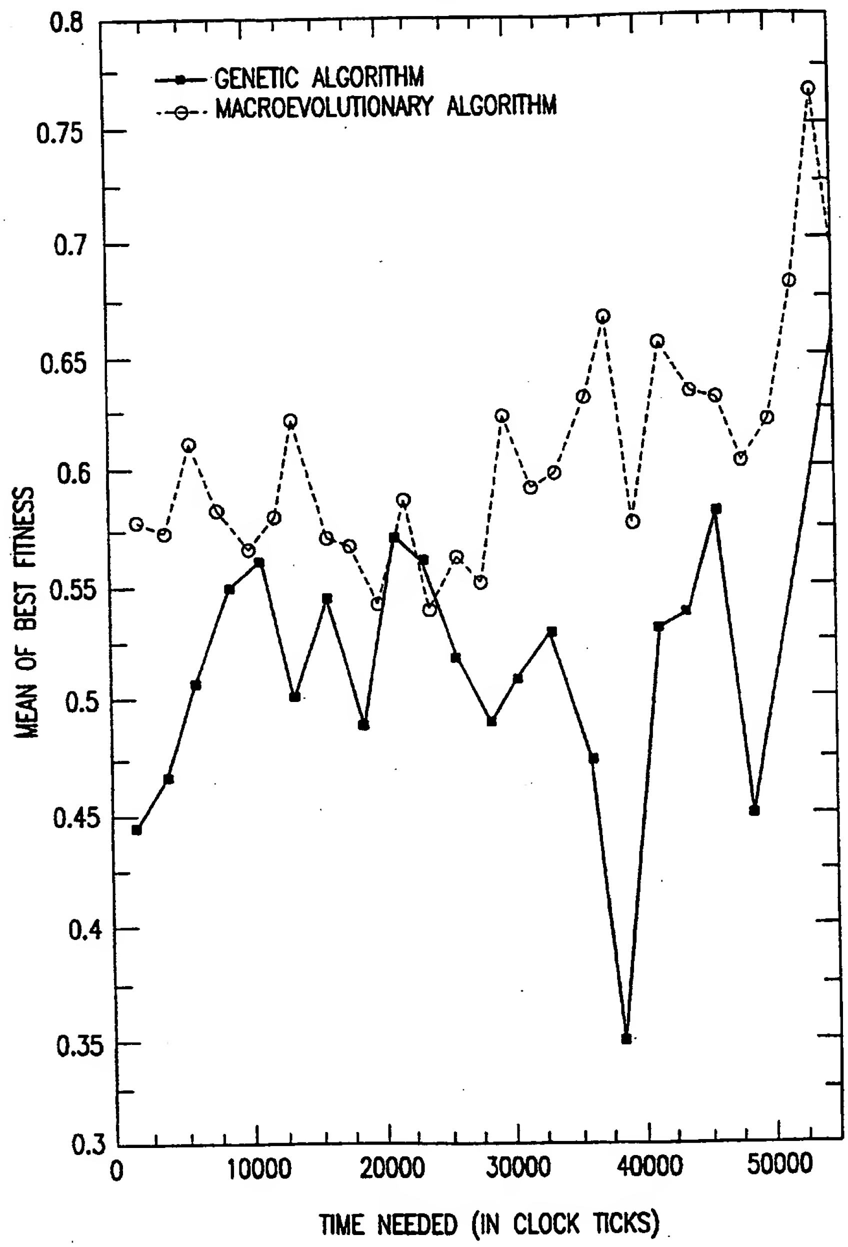
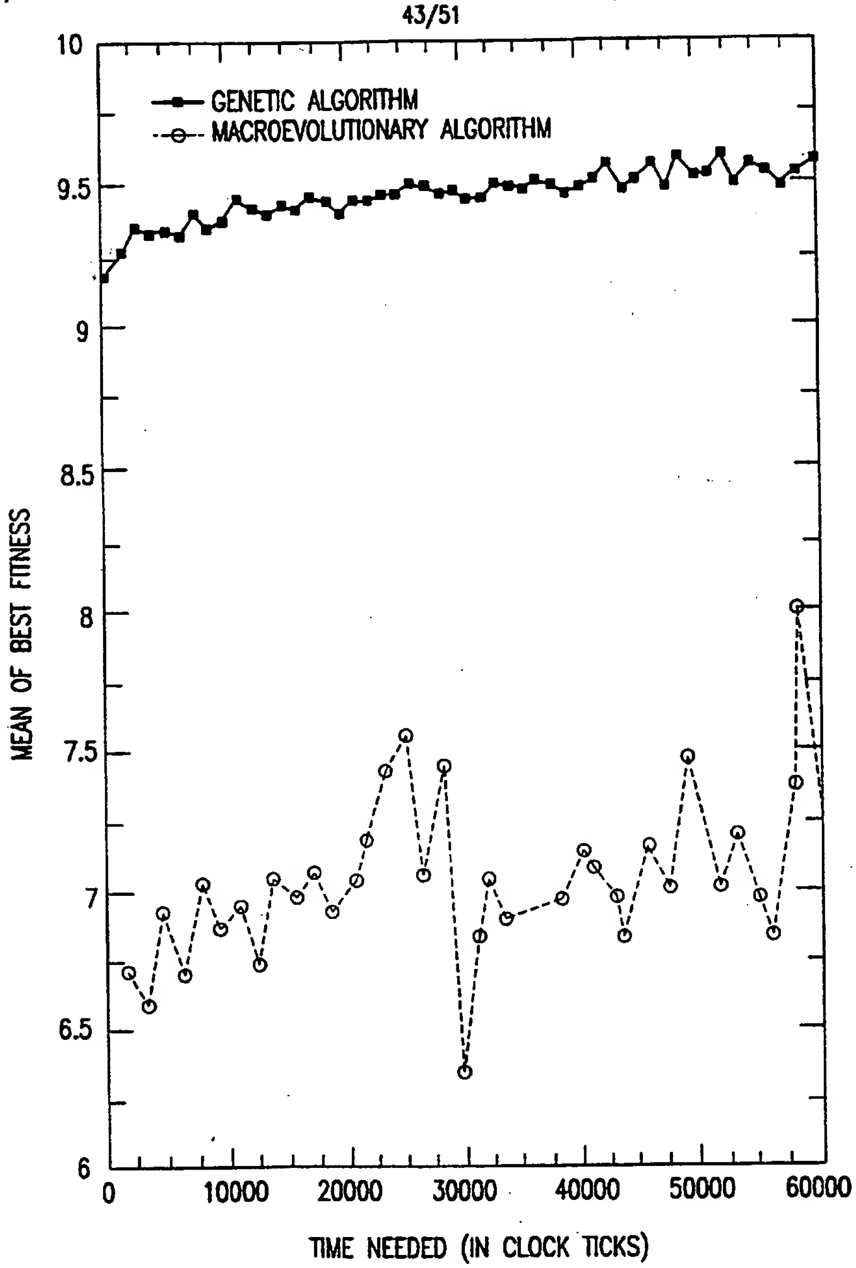

GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
MEAN OF BEST FITNESS
0.8
0.75
0.7
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
0
10000
20000
30000
40000
50000
TIME NEEDED (IN CLOCK TICKS)

FIG.9D



10
9.5
9
8.5
8
7.5
7
6.5
6
0
10000
20000
30000
40000
50000
60000
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
MEAN OF BEST FITNESS
TIME NEEDED (IN CLOCK TICKS)

FIG.10A

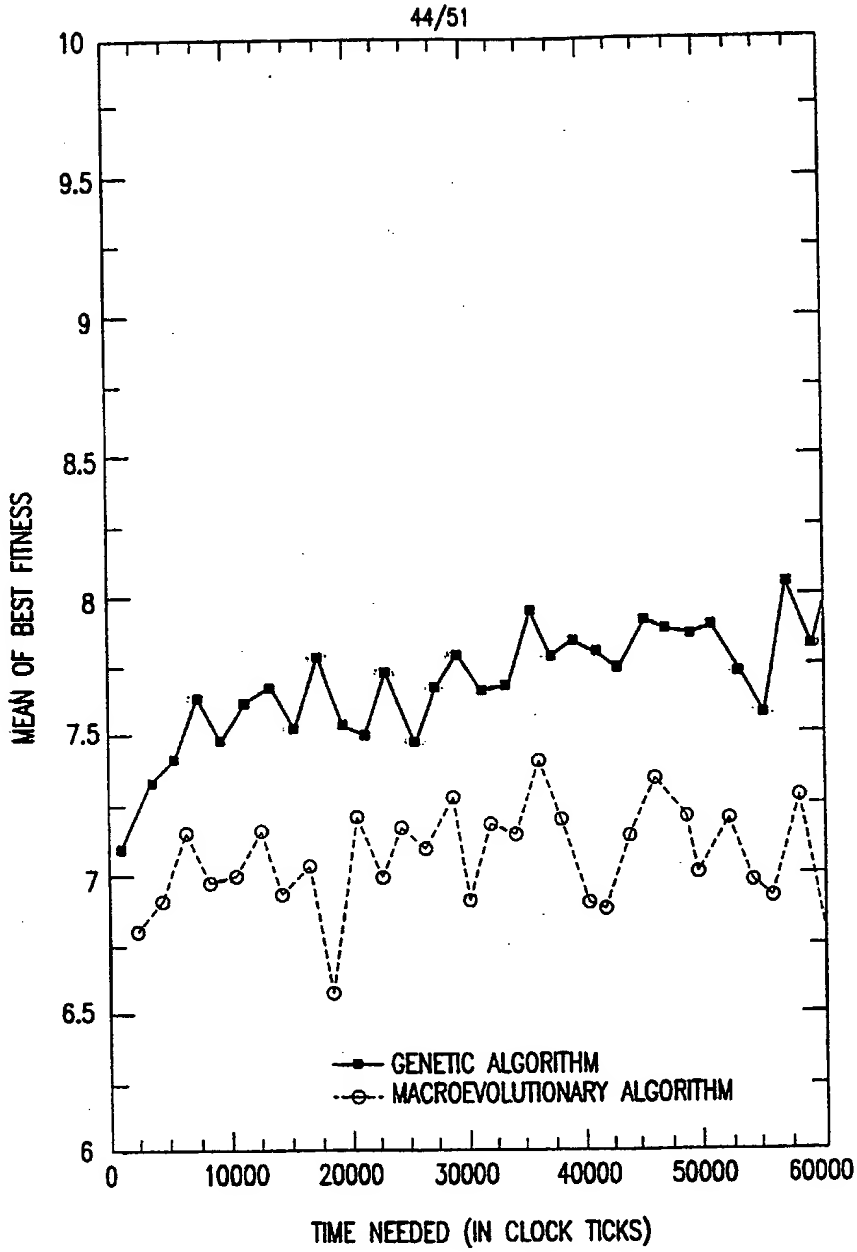
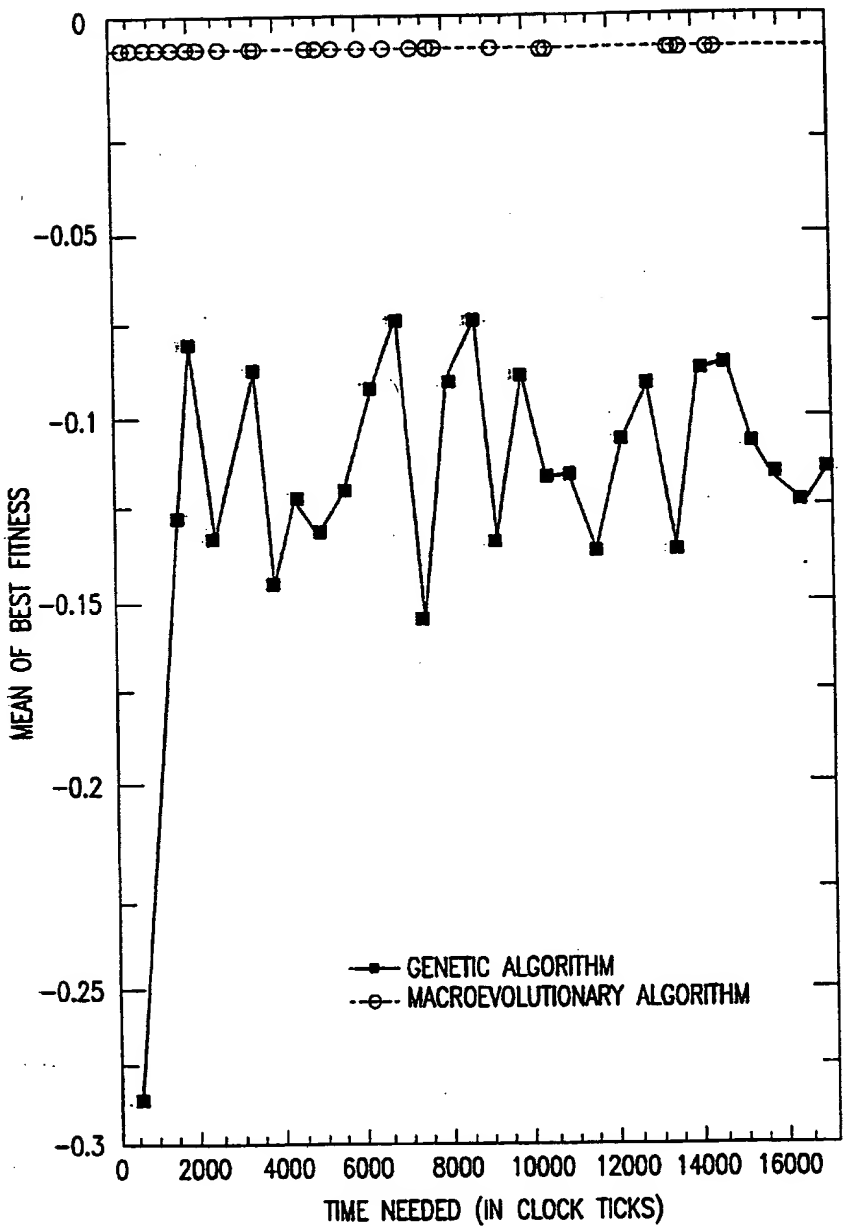

10
9.5
9
8.5
8
7.5
7
6.5
6
MEAN OF BEST FITNESS
0
10000
20000
30000
40000
50000
60000
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.10B



0
-0.05
-0.1
-0.15
-0.2
-0.25
-0.3
MEAN OF BEST FITNESS
0
2000
4000
6000
8000
10000
12000
14000
16000
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.11A

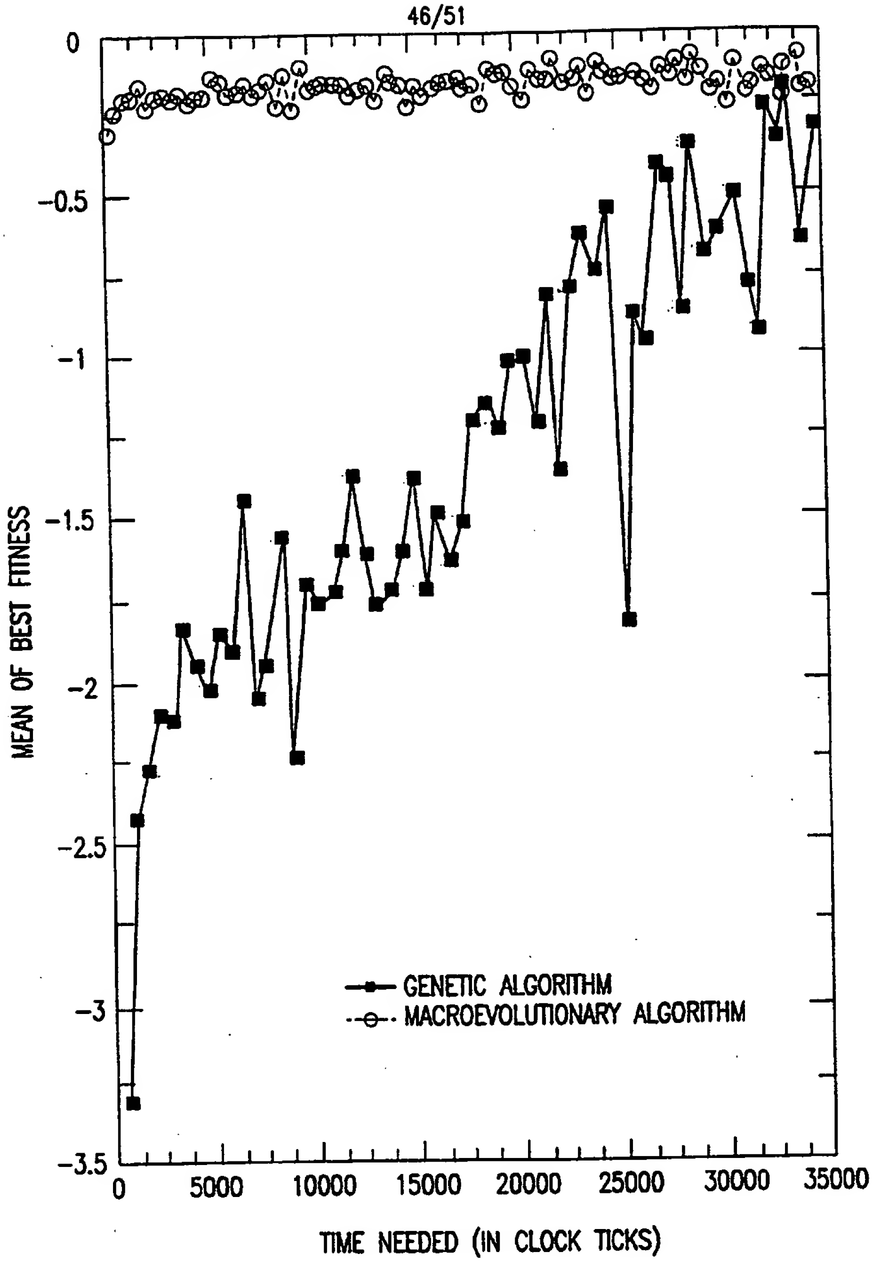

0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
0
5000
10000
15000
20000
25000
30000
35000
MEAN OF BEST FITNESS
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.11B

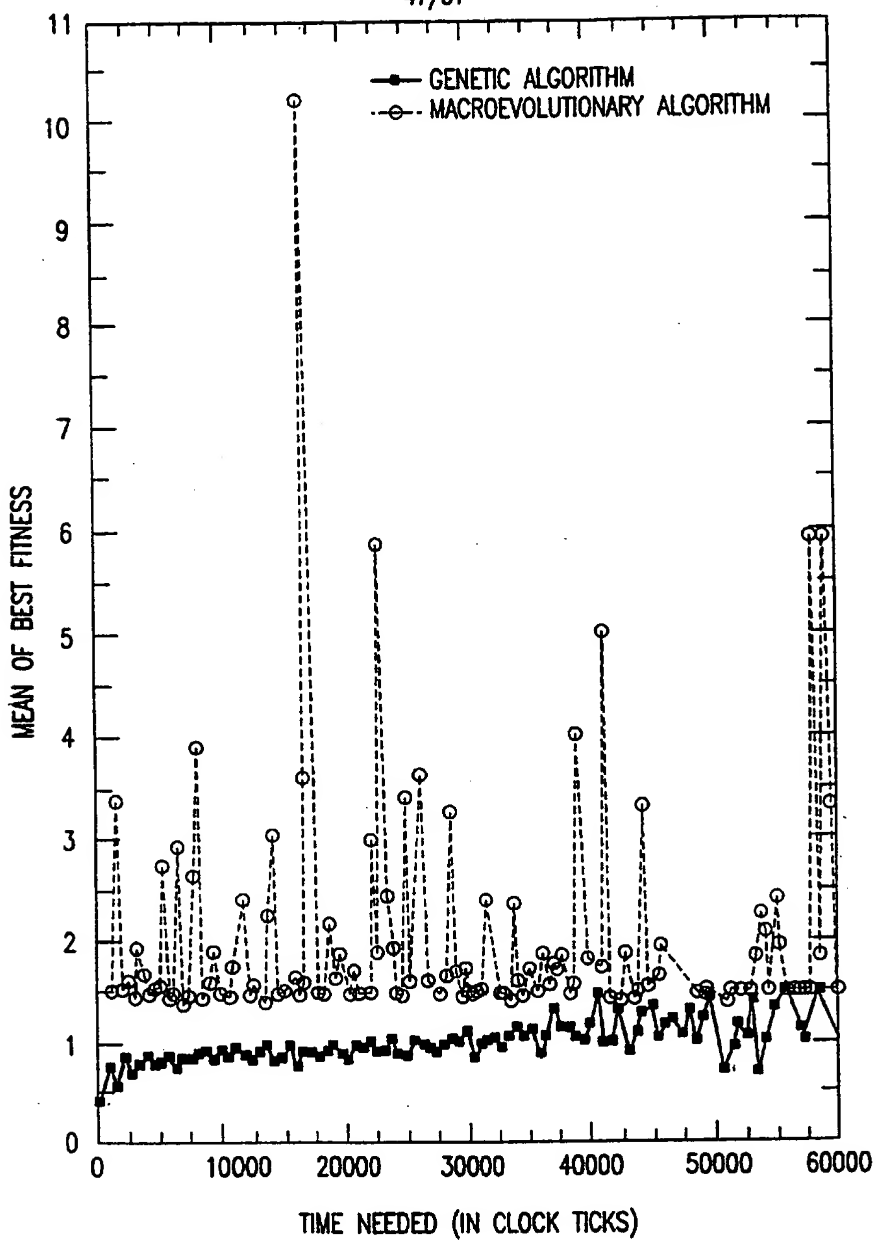

GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
MEAN OF BEST FITNESS
0
1
2
3
4
5
6
7
8
9
10
11
0
10000
20000
30000
40000
50000
60000
TIME NEEDED (IN CLOCK TICKS)

FIG.11C

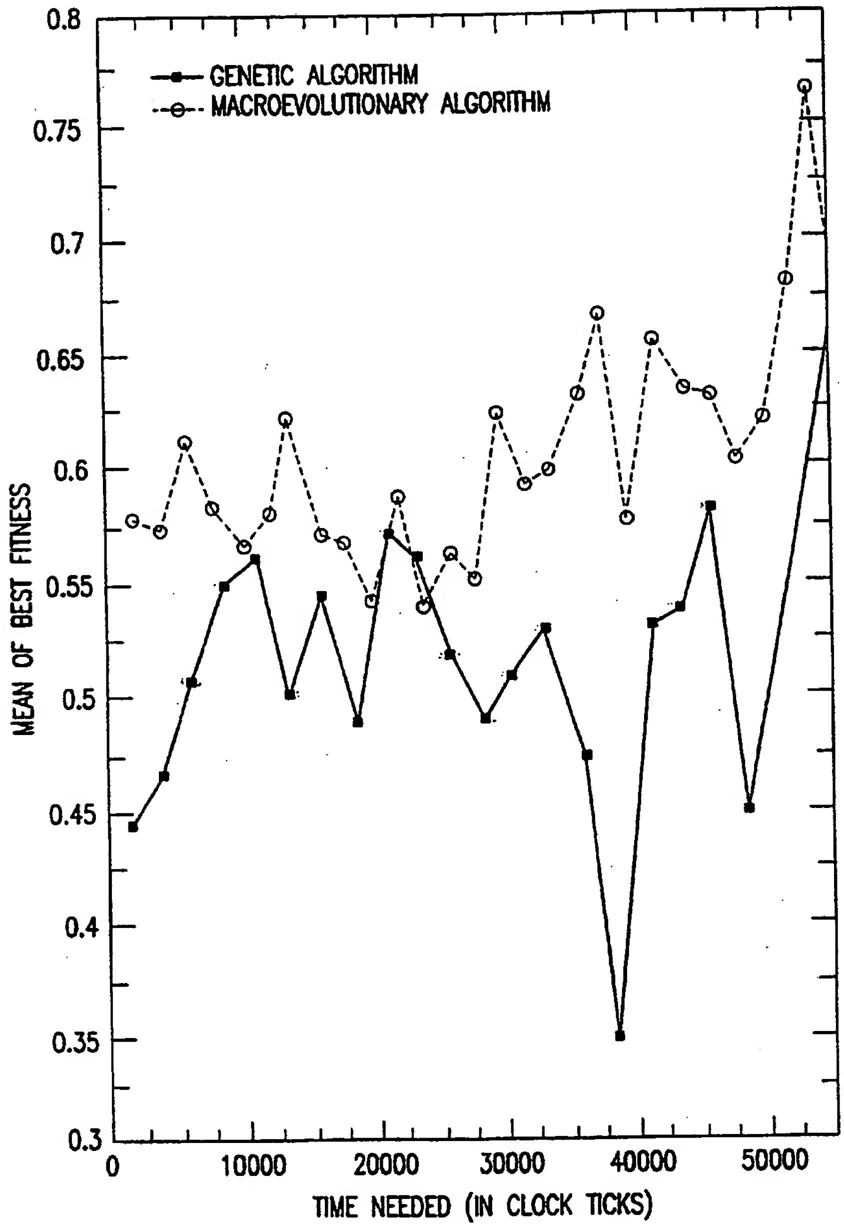
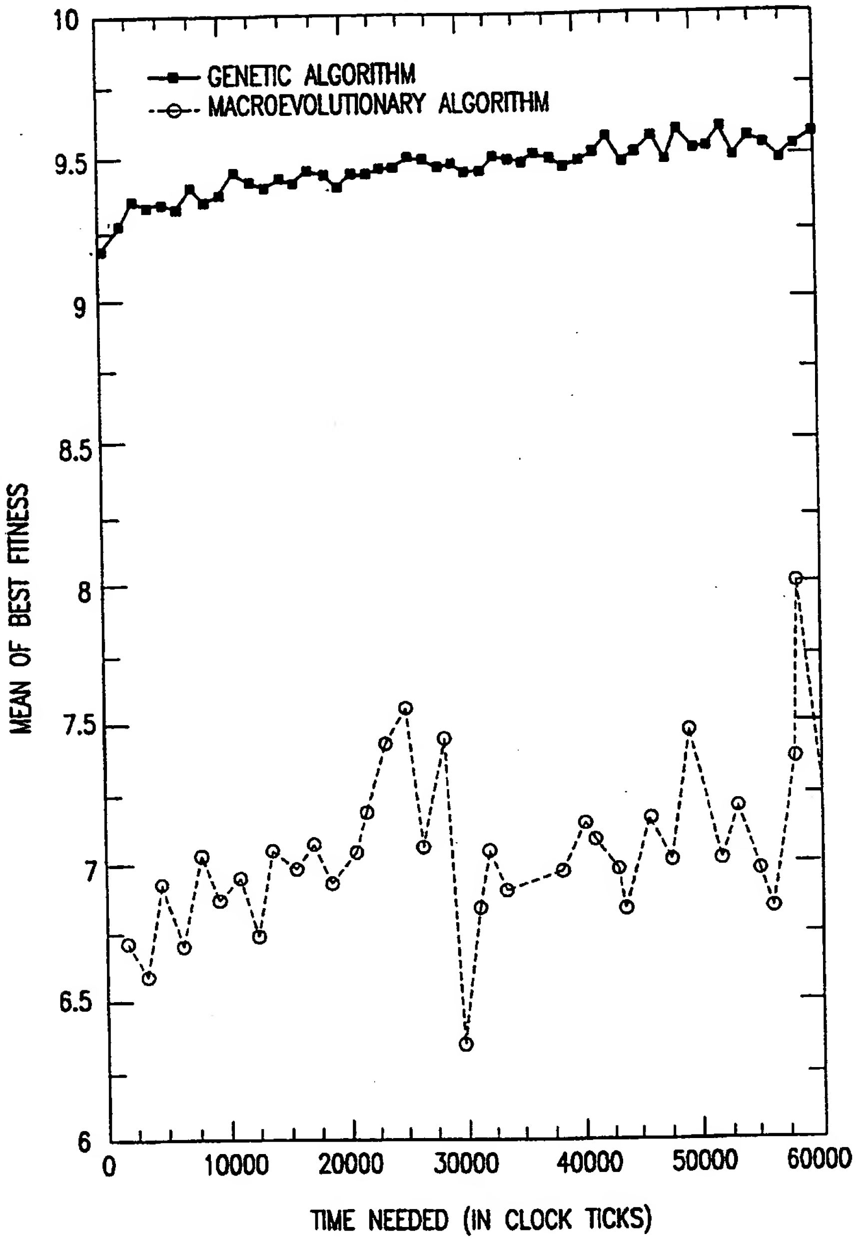

GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
MEAN OF BEST FITNESS
0.8
0.75
0.7
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
0
10000
20000
30000
40000
50000
TIME NEEDED (IN CLOCK TICKS)

FIG.11D



10
9.5
9
8.5
8
7.5
7
6.5
6
MEAN OF BEST FITNESS
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM
0
10000
20000
30000
40000
50000
60000
TIME NEEDED (IN CLOCK TICKS)

FIG.12A

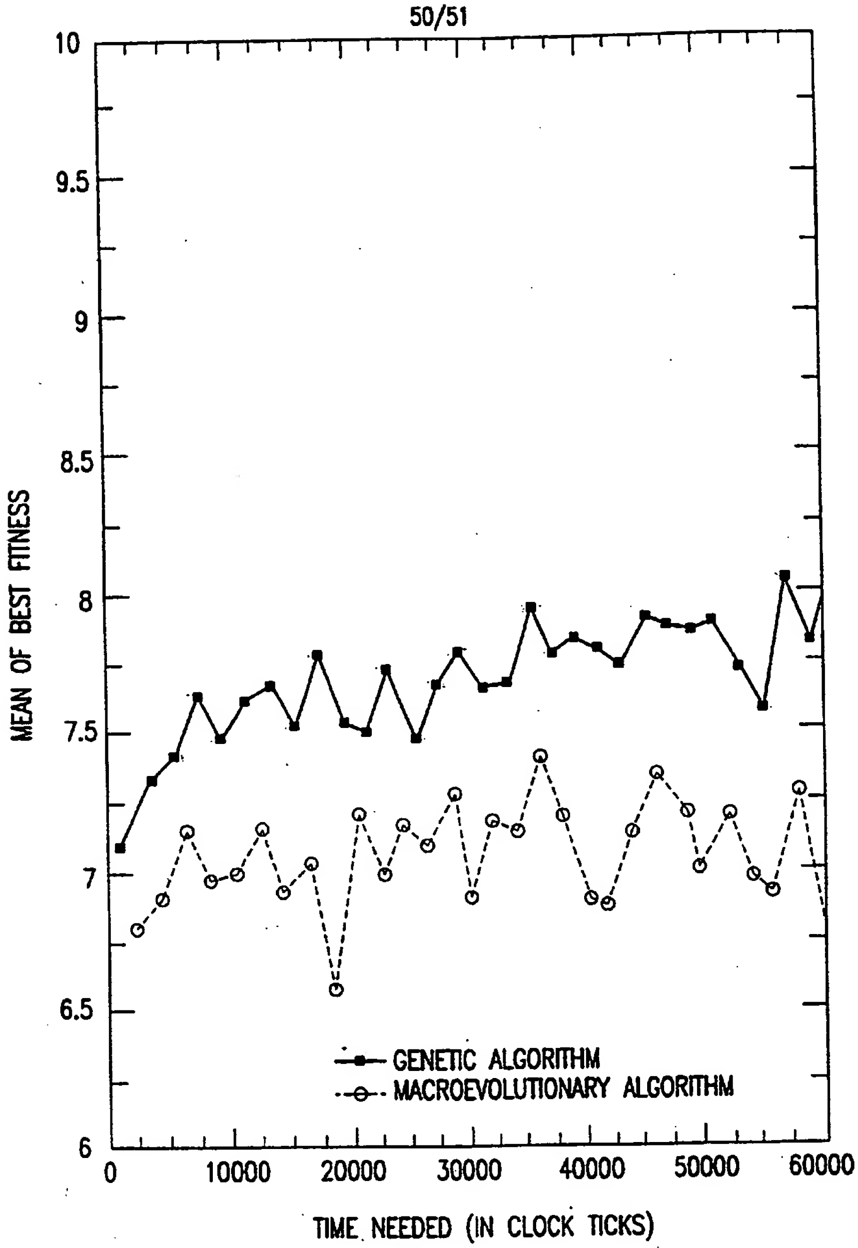

10
9.5
9
8.5
8
7.5
7
6.5
6
MEAN OF BEST FITNESS
0
10000
20000
30000
40000
50000
60000
TIME NEEDED (IN CLOCK TICKS)
GENETIC ALGORITHM
MACROEVOLUTIONARY ALGORITHM

FIG.12B

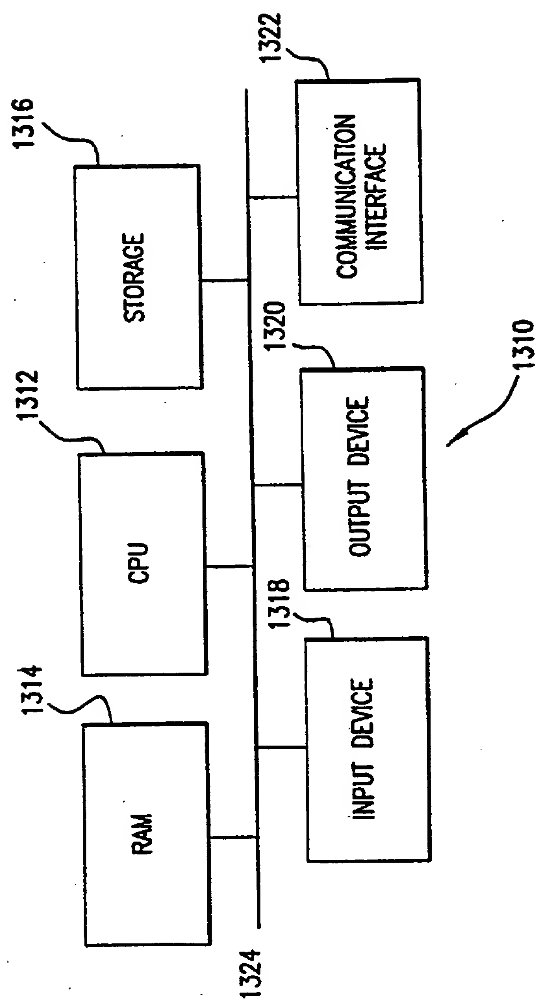

1316
STORAGE
1312
CPU
1314
RAM
1322
COMMUNICATION INTERFACE
1320
OUTPUT DEVICE
1318
INPUT DEVICE
1324
1310

FIG.13

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/30641

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :G06F 15/18
US CL :706/13, 12
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 706/13, 12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Pleas: See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	MARIN, J. et al. Macroevolutionary Algorithms: A New Optimization Method on Fitness Landscapes. IEEE Transactions on Evolutionary Computation. Novermber 1999. Vol. 3. No. 4. pp. 272-286.	1-9
X	SIBANI, P. et al. Evolution and Extinction Dynamics in a Rugged Fitness Landscapes. International Journal of Modern Physics B. 1998. Vol. 12. pp. 361-391.	1-9
A	RICE, SEAN H. A Genetic Theory of Species Selection. Journal of Theoretical Biology. December 1995. Vol. 177. No. 3. pp. 237-245.	1-9

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
10 MARCH 2000	11 APR 2000

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	JASON RHODES
Facsimile No. (703) 305-3230	Telephone No. (703) 305-3942

Form PCT/ISA/210 (second sheet) (July 1998)*

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SIBANI, P. Soluble Model of Evolution and Extinction Dynamics in a Rugged Fitness Landscape. Physical Review Letters. August 1997. Vol. 79. No. 7. pp. 1413-1416.	1-9
A	HUGHES, E.J. et al. A Multi-Species Genetic Algorithm Applied to Radar Scattering Centre Identification in Three-Dimensions. Second International Conference On Genetic Algorithms in Engineering Systems. 1997. pp. 472-477.	1-9
A	IWASAKI, Y. et al. Genetic Evolution Through Stochastic Mutation Dynamics. Proceedings of the IEEE International Conference on Evolutionary Computation. 1996. pp. 849-854.	1-9
A	POTTS, J.C. et al. The Development and Evaluation of an Improved Genetic Algorithm Based on Migration and Artificial Selection. IEEE Transactions on Systems, Man, and Cybernetics. January 1994. Vol. 24. No. 1. pp. 73-86.	1-9
A	HUANG, YO-PING et al. Genetic Algorithms in the Identification of Fuzzy Compensation System. IEEE Transactions on Systems, Man, and Cybernetics. October 1996. Vol. 2. pp. 1090-1095.	1-9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/30641

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

WEST, STN, IEEE/IEE ONLINE, ACM DIGITAL LIBRARY, ELSEVIER, ACADEMIC PRESS
search terms: macroevolution, genetic, species, network, optimize

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Search results for application number: 09/920,344

Application Filing Date:	07-31-2001	Class / Sub-Class:	705/-
Issue Date of Patent:	-	Location:	INITIAL-EXAM CENTRAL FIL
Examiner Name:	-	Status:	Application Undergoing Pre Processing
Group Art Unit:	2161	Attorney Docket Number:	11121.00
Earliest Publication No:	-	Patent Number:	-
Earliest Publication Date:	-	Customer Number:	20686
Confirmation Number:	4179		

Foreign Priority | Continuity Data | Publication Review

File Contents History

Number	Date	Contents Description
4	09-10-2001	Incomplete Application under Rule 53(b) - Filing Date Assigne
3	09-08-2001	Correspondence Address Change
2	08-08-2001	Application Scanned and Dispatched from OIPE
1	07-31-2001	Initial Exam Team nn

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